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GenCore version 5.1.6
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7, 2004, 12:53:09; Search time 62.9091 Seconds (without alignments) 71.862 Million cell updates/sec October Run on:

US-09-336-091-3 74 Title: Perfect score:

1 VKVLEYVIKVSARVRF 16 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1586107 seqs, 282547505 residues Searched:

Total number of hits satisfying chosen parameters:

1586107

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

A\_Geneseq\_29Jan04:\*
11: geneseqp1980s:\*
2: geneseqp1990s:\*
3: geneseqp2000s:\*
4: geneseqp2001s:\* geneseqp2003as:\*geneseqp2003bs:\* geneseqp2002s:\* geneseqp2004s:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Aab31291 Peptide d	Aau85042 Human MAG	Aar70909 Human mel	Aaw81548 Tumour re	Aab31290 Amino aci	Aae06806 Human MAG	Aau84814 Human MAG	Abp74195 Human MAG	Abu08930 Human tum	Adc09573 MAGE-1 pr	Aao19742 Wild-type	Abu04419 Human exp	Aay06592 CLYTA-MAG	Aay06590 Lipoprote		Aau85130 Human mel		Aab31292 Peptide d	Aab31300 Peptide d	Aay06998 MAGE-4 pr	Lung Ca	Ada83770 Human MAG	Aab08734 Amino aci	Aab31294 Peptide d	Aay38326 MAGE-deri
ΩI	AAB31291	AAU85042	AAR70909	AAW81548	AAB31290	AAE06806	AAU84814	ABP74195	ABU08930	ADC09573	AA019742	ABU04419	AAY06592	AAY06590	ABR57354	AAU85130	AAB31295	AAB31292	AAB31300	AAY06998	ABU56545	ADA83770	AAB08734	AAB31294	AAY38326
* Query Match Length DB	16 4	30 5	309 2	309 2	309 4	309 4	309 5	309 6	309 6	309 7	310 6	316 6	445 2	446 2	1052 6	3541 5	12 4	16 4	16 4	317 2	317 6	317 6	318 3	12 4	10 2
& Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	77.0	77.0	75.7	75.7	75.7	75.7	75.7	73.0	62.2
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Aar70948 Human mel Aar70957 Human mel Aar70966 Human mel	Aar70960 Human mel Aay46118 Immunogen Aay46178 Immunogen Aay46179 Immunogen				Aar78807 MAGE 1 27 Aar78907 MAGE 1 27 Aar70922 Human mel Aay47408 Immunogen
AAR70948 AAR70957 AAR70966	AAR70960 AAY46118 AAY46178 AAY4607	ABP74245 ABP74240 ADC09099	ADC09104 AAR70943 AAR70953	AAY47264 AAY46179 AAB31301	AAR 73838 AAR 78907 AAR 70922 AAY 47408
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## ALIGNMENTS

MAGE-A1; HLA; human leukocyte antigen; CD4+ T lymphocyte; cancer; MAGE-A1 HLA class II-binding protein; vaccine. Peptide derived from human MAGE-Al HLA class II-binding protein. AAB31291 standard; peptide; 16 AA. (LUDW-) LUDWIG INST CANCER RES 14-JUN-2000; 2000WO-US016287. 99US-00336091. (first entry) WO200078806-A1 Homo sapiens. 18-JUN-1999; 20-APR-2001 28-DEC-2000. AAB31291; AAB3129 

Boon-Falleur T, Chaux P, Lethe B, WPI; 2001-102698/11. Van Snick J,

Van Der Bruggen

Novel MAGE-A1 human leukocyte antigen class II peptides which bind to and are presented to the class II molecules, useful for inducing immune response and treating cancers characterized by expression of MAGE-A1.

Claim 3; Page 42; 78pp; English.

antigen) class II-binding protein. Peptides derived from the MAGE-A1 HLA binding protein stimulate the activity and proliferation of CD4+ T lymphocytes. The MAGE-A1 HLA binding protein is useful as a diagnostic agent for diagnosing a disorder characterized by expression of MAGE-A1. The protein is used for treating a disorder characterized by expression of MAGE-A1 such as cancers e.g. melanomal, squamous cell carcinomas, colorectal carcinomas, and lymphocytic leukemias. Peptides derived from the MAGE-A1 HLA binding protein are useful in the production The present sequence is derived from a human MAGE-A1 HLA (human leukocyte of anti-tumour vaccines

Sequence 16 AA;

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The invention relates to a new synthetic polypeptide (I) comprising several different segments of at least one parent polypeptide linked to together in a different relationship relative to their linkede in the parent polypeptide to impede, abrogate or otherwise alter at least one function associated with the parent polypeptide and for inducing an immune response against a pathogen or cancer. Also included are a synthetic polypeptide encoding and a computer system for designing the synthetic polypeptides. The synthetic polypeptides and polynucleotides are referred to as a Savine. The synthetic polypeptide is useful for modulating immune responses preferably directed against a pathogen or a cancer, (e.g., cancers of the lung, breast, overvix, colon, head and neck, pancreas, prostate, stomach, bladder, kidney, bone liver, cesophagus, brain, testicle, uterus), as potentitating against a comprising the polypeptide may be used in the treatment or prophylaxis against virus, hepatitis, influenza, Japanese encephalitis immunodeficiency virus), hepatitis, influenza, Japanese encephalicis (e.g., infections caused by Neisseria, Meningococcal, Haemophilus, salmonella, Streptococcal, Legionella and Mycobacterium or parasitic
                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New synthetic polypeptides having several different segments of at least one parent polypeptide linked together differently compared to the linkage in the parent polypeptide, for inducing immune response against a
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                                         Gaps
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 Length 16;
                                       Indels
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 Score 74; DB 4; I
Pred. No. 1.7e-06;
; Mismatches 0;
                                                                                                                                                                                                             AAU85042 standard; peptide; 30 AA
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     100.0%; Fr.
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   100.08;
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Query Match 100.
Best Local Similarity 100.
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                          Human MAGE-1 segment 19
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N-PSDB; ABK36862.
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Sequence 30 AA;

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                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human melanoma antigen, MAGB-1, peptide(s) - useful for stimulating immune response against melanoma.
                                                                                                                                                                                                                                                                 Human melanoma antigen; MAGE-1; vaccines; MAGE associated tumours; HLA-restricted cytotoxic T-lymphocyte activity.
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           Length 30;
                                    0; Indels
             Score 74; DB 5;
Pred. No. 3.3e-06;
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                                    Mismatches
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                                                                                                                                                   AAR70909 standard; protein; 309 AA.
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             100.0%;
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Query Match
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Best Local 16; Conservative
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Matches 16, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                  02-AUG-1994;
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09-OCT-1995
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                                                                                                                                                                            AAR70909;
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The present sequence represents a human MAGE-A1 HLA (human leukocyte antigen) class II-binding protein. Peptides derived from the MAGE-A1 HLA binding protein atimulate the activity and proliferation of CD4+ T lymphocytes. The MAGE-A1 HLA binding protein is useful as a diagnostic agent for diagnosing a disorder characterized by expression of MAGE-A1. The protein is used for treating a disorder characterized by expression of MAGE-A1 coch as cancers e.g. melanomal, squamous cell carcinomas, of endanced actinomas, osteosarcomas, and lymphocytic leukemias. Peptides derived from the MAGE-A1 HLA binding protein are useful in the production
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                                                                                                                       Novel MAGE-A1 human leukocyte antigen class II peptides which bind to are presented to the class II molecules, useful for inducing immune response and treating cancers characterized by expression of MAGE-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAGE antigenic peptide; Human leukocyte antigen; HLA-B35; HLA-B44; tumour cell; immunostimulant; antigen presentation; cancer; melanoma; CD8+ cytotoxir T lymphocyte; colorectal; prostate; gastric carcinoma; myeloma; brain tumour; sarcoma; seminoma; ovarian tumour; cytostatic; gene therapy; human; MAGE-A1; tumour rejection antigen; TRA.
                     Van Der Bruggen P;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 309;
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100.0%; Pred. No. 4.5e-05;
.ive 0; Mismatches 0; Indels
                     Boon-Falleur T,
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                     Chaux P,
                                                                                                                                                                                                            Claim 1; Page 63; 78pp; English.
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25-OCT-2000; 2000US-0243212P.
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Best Local Similarity 100.
Matches 16; Conservative
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                     Lethe B,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-488724/53.
                                                            WPI; 2001-102698/11
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                     Snick J,
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Demotte N,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   precursor (TRAP) MAGE-A1. MAGE-A1 cDNA (see ANG9719) shows homology to novel human MAGE-C1 cDNA (see ANG8720). MAGE-C1 (see AAW81546) is a novel member of the MAGE family that may be recognised by cytotoxic T cells, leading to lysis of the tumour cells which express it. It is expressed in a variety of tumours and in normal testis cells, but not by other normal cells. The invention provides MACE-C1 and MAGE-C2 nucleic acids and polypeptides, useful e.g. in a claimed method for determining the presence of cytolytic T cells specific for complexes of a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                              rejection antigen precursors - used for determining presence of ic T cells specific for complexes of a human leukocyte antigen.
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                                       MAGE-A1; human; tumour rejection antigen precursor; TRAP; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amino acid sequence of human MAGE-Al HLA class II-binding protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This is the amino acid sequence of human tumour rejection antigen
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Tumour rejection antigen precursor MAGE-A1.
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                                                                                                                                                                                                                                                                                                                                                        Boon-Falleur T;
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Best Local Similarity 100.
Matches 16; Conservative
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                                                                                                                                                                                                                                                                       25-APR-1997;
                                                                                                                                           WO9849184-A1
                                                                                                                                                                                                                              24-APR-1998;
                                                                                                      domo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                    05-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-DEC-2000
                                                            diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB31290;
                                                                                                                                                                                                                                                                                                                                                        Lucas S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 5
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cell.
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                                         The invention relates to functional variants and isolated mimetics of a MAGE-A1 human leukocyte antigen (HLA)-B35 or HLA-B44 binding peptide, or of a MAGE-A1 human leukocyte antigen (HLA)-B35 or HLA-B44 binding peptide, or the specification. MAGE genes encode tumour rejection antigens (TRAA) presented to T lymphocytes by HLA-B35 and HLA-B44 molecules. The MAGE antigenic peptide acts by binding to HLA molecules on tumour cells and stimulating recognition of these cells and thus signalling them to the immune system for destruction. The peptide when presented by HLA molecule induces the activation and stimulation of CD8+ cytotoxic T lymphocytes. The MAGE antigenic peptide is used to treat and diagnose disorders characterised by expression of MAGE-A1 or -A3. Disorders include cancers commense, oesophageal, lung, head and neck, breast, colorectal, prostate, renal, bladder, hepatocellular, papillary thyroid and gastric carcinomas, myelomas, brain tumours, sarcomas, seminomas, and ovarian tumours. The present sequence is human MAGE-A1 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New synthetic polypeptides having several different segments of at least one parent polypeptide linked together differently compared to the linkage in the parent polypeptide, for inducing immune response against a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a new synthetic polypeptide (I) comprising several different segments of at least one parent polypeptide linked together in a different relationship relative to their linkage in the parent polypeptide to impede, abrogate or otherwise alter at least one function associated with the parent polypeptide and for inducing an
                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus; viral infection; human immunodeficieny virus; melanoma; bacterial infection; Salmonella; Legionella; parasitic infection;
                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                      Length 309;
                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 74; DB 4; I 100.0%; Pred. No. 4.5e-05; iive 0; Mismatches 0;
             Claim 2; Page 86-87; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU84814 standard; protein; 309 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 3; Fig 27; 364pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Trypanosoma; Toxoplasma; Giardia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human MAGE-1 consensus sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      277 VKVLEYVIKVSARVRF 292
                                                                                                                                                                                                                                                                                                                                                                                                                     1 VKVLEYVIKVSARVRF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-MAY-2001; 2001WO-AU000622.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-MAY-2000; 2000AU-00007761.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AUSU ) UNIV AUSTRALIAN NAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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Best Local Similarity 100.0
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ramshaw IA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-147575/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pathogen or cancer.
                                                                                                                                                                                                                                                                                                                     Sequence 309 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200190197-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thomson SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU84814;
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immune response against a pathogen or cancer. Also included are a synthetic polypeptides encoding and a computer system for designing the synthetic polypeptides. The synthetic polypeptides and polynucleotides are referred to as a Savine. The synthetic polypeptide is useful for modulating immune responses preferably directed against a pathogen or a cancer, (e.g., cancers of the lung, breast, ovary, cervix, colon, head and neck, pancreas, prostate, stomach, bladder, kidney, bone liver, cosophagus, brain, testicle, uterus), as potentiating agents.

Compositions comprising the polypeptide may be used in the treatment or prophylaxis against virus), hepatitis, influenza, Japanese encephalitis virus, bestein-Barr virus and respiratory syncytial virus), bacterial (e.g., infections caused by Neisseria, Meningococcal, Haemophilus, Salmonella, Streptococcal, Legionella and Mycobacterium or parasitic (e.g., infections caused by Plasmodium, Schistosoma, Leishmania, Trypanosoma, Toxoplasma and Giaddia) infections. The present sequence is a consensus sequence for a parent protein used to design a savine of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; epitope; vaccine; immunotherapeutic; cytostatic; immunogenicity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes an isolated epitope (1) and an epitope cluster. Also described is a vaccine or immunotherapeutic composition (VC) comprising (1). (1) has cytostatic activity. VC is useful for treating an animal, by administering to an animal, by administering to an animal the vaccine or immunotherapeutic composition. VC is also useful for evaluating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel epitopes useful as vaccines, comprises peptides or nucleic acid encoding the peptides, that are useful epitopes of target-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 74; DB 5; Length 309; 100.0%; Pred. No. 4.5e-05; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liu L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CTLI-) CTL IMMUNOTHERAPIES CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                277 VKVLEYVIKVSARVRF 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-APR-2002; 2002WO-US011101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 VKVLEYVIKVSARVRF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-APR-2001; 2001US-0282211P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-NOV-2001; 2001US-0337017P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Simard JJL, Diamond DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-067518/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ABQ83847.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 309 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                invention
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immunogenicity of a vaccine or immunotherapeutic composition, by administering VC to an HIA-transgenic animal and evaluating immunogenicity based on a characteristic of the animal. or by in vitro primary stimulation of a T cell and evaluating immunogenicity. (I) is useful for determining specific T cell frequency, by contacting T cells with a MHC-peptide complex, and further comprises BLISPOT analysis, polymerase chain reaction (FRC. Ago83843 to ABQ83858 and ABP74128 to ABD74113 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRAP; tumour rejection antigen precursor; cytolytic T-cell; CTL; tumour; seminoma; bladder transitional-cell carcinoma; NSCLC; adaptor; head-and-neck squamous-cell carcinoma; breast carcinoma; sarcoma; cutaneous melanoma; nonsmall cell lung cancer; MAGE-A1; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated nucleic acid encoding tumor rejection antigen precursor MAGE-C3, MAGE-B5, or MAGE-B6, useful as diagnostic probes to determine presence of abnormal e.g., tumor cells expressing MAGE-C1, MAGE-B5 or
                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                         100.0%; Score 74; DB 6; Length 309; 100.0%; Pred. No. 4.5e-05;
                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human tumour rejection antigen precursor, MAGE-A1.
                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                ABU08930 standard; protein; 309 AA.
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                                                                                                                                                                                                                                                                                                                                       277 VKVLEYVIKVSARVRF 292
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24-APR-1998; 98US-00066281.
17-DEC-1999; 99US-00468433.
09-FEB-2000; 2000US-00501104.
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                                                                                                                                                                                                                                                                                                                  1 VKVLEYVIKVSARVRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Boon-Falleur T;
                                                                                                                                                                                                                                                          Local Similarity 100.
Les 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (LUCA/) LUCAS S.
(BOON/) BOON-FALLEUR T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-328468/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ABX93696
                                                                                                                                                                                                         Sequence 309 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US2002176865-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-NOV-2002
                                                                                                                                                                    invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lucas S,
                                                                                                                                                                                                                                         Query Match
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Matches
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ABU08930
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             head-and-neck squamous-cell carcinoma, breast carcinoma, sarcoma, cutaneous melanoma or nonsmall cell lung cancer (NSCLC) which express MAGE-C1. MAGE-B5 or MAGE-B6. The nucleic acid is useful for diagnoshing a disorder characterised by expression of MAGE-C1, MAGE-B5 or MAGE-B6 TRAPs or tumour rejection antigens (TRAS). The present sequence represents the amino acid sequence of the human tumour rejection antigen MAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated epitope polypeptide that has high affinity for major histocompatibility complex (MHC) class I, and an epitope cluster comprising the polypeptide. Also disclosed is a vaccine or immunotherapeutic composition containing an epitope of the invention. Compositions of the invention may be used in the treatment of cancer. The method can be combined with a radiation therapy, chemotherapy biochemotherapy or surgery. The composition is also useful for evaluating immunogenicity of a vaccine or immunotherapeutic compound. Multimeric Peptide complexes of the invention are useful for determining specific T response, by performing the method is useful for evaluating immunological response, by performing the method prior to and subsequent to an immunisation step. Compositions of the invention are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complex class of a vaccine or
                                                                                                                                                                                                                                     Gaps
cells such as seminoma, bladder transitional-cell carcinoma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diagnosing a disease. The current sequence represents an epitope of invention with high affinity for MHC class I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Epitope; immunological; vaccine;
major histocompatibility complex class I; MHC class I; cancer;
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                                                                                                                                                                                               Length 309;
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                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            therapeutic composition and for diagnosing a disease
                                                                                                                                                                                               100.0%; Score 74; DB 6; I
100.0%; Pred. No. 4.5e-05;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                   ADC09573 standard; protein; 309 AA.
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                                                                                                                                                                                                                                                                                          277 VKVLEYVIKVSARVRF 292
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07-NOV-2001; 2001US-0337017P.
07-MAR-2002; 2002US-0363210P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                       1 VKVLEYVIKVSARVRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MAGE-1 protein #SEQ ID 71
                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Diamond DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-248010/24.
                                                                                                                                                             Sequence 309 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immuni sation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified
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 (tumour)
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Translational profiling, expressed protein tag; EPT; kinase; phosphatase; protease; protease inhibitor; transporter; cytoskeletal protein; receptor; transcription factor; cancer; MHC; major histocompatability complex; myeloma; colon cancer; gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polypeptides (e.g. kinases, phosphatases, proteases, transporters, cytoskeletal proteins, receptors or transcription factors), useful for treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or leukemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2; SEQ ID NO 1085; 134pp; English.
                                                                                                         Human expressed protein tag (EPT) #1085.
ABU04419 standard; protein; 316 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tomlinson AJ, Urban RG;
                                                                                                                                                                                                                                                                                                                                                                                                28-MAR-2001; 2001US-0279495P.
21-MAY-2001; 2001US-0292544P.
08-AUG-2001; 2001US-0316801P.
01-OCT-2001; 2001US-0336370P.
04-DEC-2001; 2001US-0336780P.
20-FEB-2002; 2002US-0358985P.
                                                                                                                                                                                                                                                                                                                                                                28-MAR-2002; 2002WO-US009671
                                                                       (first entry)
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                                                                                                                                                                                                                                                                                        WO200278524-A2
                                                                                                                                                                                                                                                        Homo sapiens.
                                                                       29-JAN-2003
                                                                                                                                                                                                                                                                                                                            10-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chicz RM,
                                   ABU04419;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a pharmaceutical composition containing at least one modified RNA encoding a biologically active or antigenic protein. The RNA is modified to optimise translation of the sequence. The compositions are used for vaccination against a wide range of infectious diseases (viral, bacterial or protozoal) or cancer, or for tissue regeneration, e.g. in cases of Alzheimer's or Parkinson's diseases and arthritis, but also to express proteins such as dystrophins, chloride ion channels (for treating cystic fibrosis) and enzymes (either for treating metabolic disorders or for synthesis of neurotransmitters such as dopamine). The present sequence is the wild-type MAGEI protein
                                                                                                                                                                                                                                                                                                                                                                           Stabilised mRNA, translation optimised; vaccine, tissue repair; sequence modification determination; gene therapy; cytostatic; virucide; antibacterial; protozoacide; nootropic; neuroprotective; infection; antiparkinsonian; immunostimulant; cancer; MAGE1 protein.
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                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Composition containing mRNA modified for optimal translation and stability, useful for treating e.g. tumors or infections, comprises increased G/C content and fewer rare codons.
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                                100.0%; Score 74; DB 7; Length 309; 100.0%; Pred. No. 4.5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 74; DB 6; Length 310; 100.0%; Pred. No. 4.5e-05;
                                                                   0; Indels
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                                                                                                                                                                                                                                    AA019742 standard; protein; 310 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 2B; 75pp; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUN-2001; 2001DE-01027283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Von Der Muelbe F, Hoerr I,
                                                                                                                                                                                                                                                                                                       (first entry)
                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (VMUE/) VON DER MUELBE F.
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                                                                                                                                                                                                                                                                                                                                           Wild-type MAGE1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-148621/14.
N-PSDB; ABZ69107.
                                               Local Similarity
es 16; Conserv
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les 16; Conserv
Sequence 309 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200298443-A2.
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                                                                                                                                                                                                                                                                    AA019742;
                                 Query Match
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Matches
                                                                     Matches
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The invention describes a purified polypeptide, which comprises a fragment of a kinase, phosphatase, protease, protease inhibitor, transporter, cytoskeletal protein, receptor or transcription factor. The polypeptide is useful as an immunogenic composition for eliciting in a mammal an immunogenic response directed against any of the purified polypeptide. The purified polypeptide, or the antibody that binds to this polypeptide, is useful for treating cancer. The polypeptide is also useful for identifying compounds that binds to a naturally processed class I or class II MHC-binding polypeptide. The polypeptides and polymelectides are particularly useful for treating or preventing
                                                                                                                                                                                                                                                                                                                                                                                                   myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, lymphoma or leukaemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an expressed protein tag (EPT) isolated from human tissue for translational profiling. Note: This sequence does not appear in the printed specification but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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RESULT 13 AAY06592

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RESULT 12

ABU04419

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The present sequence represents a novel fusion protein composed of lipidated protein D (LPD) of Haemophilus influenzae B, the human MAGE-1 tumour-associated antigen and amexahistidine tail. The invention relates to MAGE proteins fused to an immunological fusion partner such as LPD. The LPD moiety provides the fusion protein with additional exogenous T-cell epitopes and also increase expression levels in E. coli. The lipid tail ensures optimal presentation of the antigen to antigen-presenting cells. The affinity tag facilitates purification. The novel fusion proteins provide vaccines for immunotherapy of melanomas or other MAGE-associated tumours like breast, bladder, lung and non-small cell lung cancer, head and squamous cell carcinoma, colon carcinoma and oesophagus
                                                                                                                                                                                                                                                                                                                                                                                                                        New protein derivatives used in cancer vaccine therapy for treating a range of cancers including melanomas, carcinomas and cancers of breast.
   breast cancer; bladder cancer; lung cancer; besophagus carcinoma; head and squamous cell carcinoma; colon cancer; oesophagus carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antigen presenting cell; vaccination; nootropic; neuroprotective; antiarteriosclerotic; cytostatic; antidiabetic; hepatotropic; antiinflammatory; antiparasitic; fungicide; antibacterial; virucide; vaccine; Alzheimer's disease; atherosclerosis; cancer; diabetes; hepatitis; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 100.0%; Score 74; DB 2; Length 446; Best Local Similarity 100.0%; Pred. No. 6.7e-05; Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                     Cabezon Silva T, Cohen J, Slaoui MM, Vinals Bassols
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MatDC16-C-gamma-4-MAGE-A1 amino acid sequence.
                                                                                                                                                                                                                                                                                                    (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 6; Page 67-68; 72pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABR57354 standard; protein; 1052 AA.
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                                                                   Haemophilus influenzae,
                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-494293/41.
                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAX87591
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                                    vaccine; human.
                                                                                   Homo sapiens.
Synthetic.
                                                                                                                                                    WO9940188-A2
                                                                                                                                                                                                                     02-FEB-1999;
                                                                                                                                                                                                                                                     05-FEB-1998;
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                                                                                                                                                                                     12-AUG-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                carcinoma
                                                                                                                    Chimeric.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents a fusion protein composed of the C-terminal portion of the Streptococcus pneumoniae LYTA protein (CIVTA), the human MAGE-1 tumour-associated antigen and a hexahistidine tail. A vector designed for recombinant expression of the fusion protein in Scherichia coli is provided. The CIVTA moiety provides expression of soluble fusion protein, facilitates affinity purification, and also acts as a T-helper epitope. The invention relates to MAGE proteins fused to an immunological fusion partner, e.g. CLVTA-MAGE-1-His. These novel fusion proteins provide vacchnes for immunocherapy of melanomas or other MAGE-associated tumours like breast, bladder, lung and non-small cell lung cancer, head and squamous cell carcinoma, colon carcinoma and oesophagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAGE-1; lipoprotein D; LPD-MAGE-1-His; fusion protein; tumour; melanoma;
                                                                                                                              MAGE-1; CLYTA-MAGE-1-His; fusion protein; tumour; melanoma;
breast cancer; bladder cancer; lung cancer; colon cancer;
head and squamous cell carcinoma; oesophagus carcinoma; vaccine; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New protein derivatives used in cancer vaccine therapy for treating a range of cancers including melanomas, carcinomas and cancers of breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cabezon Silva T, Cohen J, Slaoui MM, Vinals Bassols C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lipoprotein D-MAGE-1-His fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                      (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 9; Page 69-70; 72pp; English
AAY06592 standard; protein; 445 AA.
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                                                                                                CLYTA-MAGE-1-His fusion protein.
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                                                                                                                                                                                                                                                                                                                                                                                      98GB-00002543.
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                                                                 (first entry)
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                                                                                                                                                                                                     Streptococcus pneumoniae.
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Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-494293/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAX87593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 445 AA;
                                                                 26-OCT-1999
                                                                                                                                                                                                                                                                                     WO9940188-A2
                                                                                                                                                                                                                     Homo sapiens
Synthetic.
                                                                                                                                                                                                                                                                                                                                                     02-FEB-1999;
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                                                                                                                                                                                                                                                    Chimeric.
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                                AAY06592;
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100.0%; Score 74; DB 6; Length 1052; 100.0%; Pred. No. 0.00017; tive 0; Mismatches 0; Indels C

Best Local Similarity 100.0%; Pred. No. 0.0 Matches 16; Conservative 0; Mismatches

Query Match

Search completed: October 7, 2004, 15:13:01 Job time : 64.9091 secs

1 VKVLEYVIKVSARVRF 16 |||||||||||||| 1020 VKVLEYVIKVSARVRF 1035

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sequence 143, App Sequence 11, Appli Sequence 123, App Sequence 123, App Sequence 6182, App Sequence 63, Appli Sequence 15, App Sequence 115, App Sequence 115, App Sequence 1195, App Sequence 11934, Appli Sequence 11934, Appli Sequence 11934, Appli Sequence 11934, Appli Sequence 11934, Appli

Sequence Sequence Sequence Sequence

Sequence 6929, Ap Sequence 6930, Ap Sequence 186286, Sequence 8, Appli Sequence 63003, A

Sequence Sequence

128, App 201197,

Sequence Sequence Sequence

Title: Perfect score:

Sequence:

OM protein

Run on:

Minimum DB E Maximum DB E

Database

Searched:

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Sequence 1278, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INPORMATION:
; APPLICANT: Thompson, Scott A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT FILING DATE: 2003-08-04
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 30;
                                                                                                                                                                                                                US-10-149-138-4195
US-10-149-138-4195
US-10-296-749-1280
US-10-282-122A-44745
US-10-369-493-10934
US-10-477-963-145378
US-10-437-963-145378
US-10-117-937-128
                                                                                                                                                                                                                                                                                                                                                     US-10-437-963-201197
US-10-335-977-6929
US-10-335-977-6930
US-10-424-599-186286
            US-10-117-937-124
US-10-117-937-129
US-10-128-711-84
US-10-128-711-143
US-10-150-797-1
US-10-117-937-113
US-10-117-937-123
US-10-117-937-123
US-10-149-135-2182
US-09-935-476-6
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                                                                                                                                                               US-10-128-711-93
US-10-128-711-152
US-10-150-797-13
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; OTHER INFORMATION: MAGE-1 segment 19
US-10-296-734-1278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09766889A
Patent No. US2002010164654A1
GENERAL INFORMATION:
APPLICANT: Luiten, Rosalie
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ORGANISM: Artificial
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Matches 16; Conserv
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Query Match
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equence 2, Appli
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Sequence 828, App
Sequence 10, Appl
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                                                                                                          October 7, 2004, 15:30:52; Search time 59.6364 Seconds (without alignments) 86.336 Million cell updates/sec
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Sequence 10,
Sequence 71,
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Sequence
Sequence
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(cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
(cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
(cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
(cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
(cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
(cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
(cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
(cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
(cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
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(cgn2_6/ptodata/1/pubpaa/USO09_PUBCOMB.pep:*
(cgn2_6/ptodata/1/pubpaa/USO09_PUBCOMB.pep:*
(cgn2_6/ptodata/1/pubpaa/USO09_PUBCOMB.pep:*
(cgn2_6/ptodata/1/pubpaa/USO009_PUBCOMB.pep:*
(cgn2_6/ptodata/1/pubpaa/USO009_PUBCOMB.pep:*
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(cgn2_6/ptodata/1/pubpaa/USO008_PUB.pep:*
(cgn2_6/ptodata/1/pubpaa/USO008_PUB.pep:*
            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-76-889A-2
US-09-76-889A-2
US-09-734-828
US-10-085-108-10
US-10-117-930-18
US-10-117-937-71
US-10-117-937-71
US-10-171-466-6
US-10-741-466-8
US-10-741-746-8
US-10-741-748-33
US-10-164-121A-33
                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                   1351062 segs, 321799191 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Published Applications AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                             - protein search, using sw model
                                                                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                1 VKVLEYVIKVSARVRF 16
                                                                                                                                                                                                                                                                                                                                                                        seq length: 0
seq length: 200000000
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Match Length DB
                                                                                                                                                                               US-09-336-091-3
74
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Gaps

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Score

44444444444

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; Sequence 18, Application US/10177390
; Publication No. US2003143743A1
; GENERAL INFORMATION:
    APPLICANT: Schuler, Gerold
; APPLICANT: N.V. Antwerps Innovatiecentrum
; TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
; TITLE OF INVENTION: Polynucleotides by Electroporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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100.0%; Pred. No. 8e-05;
cive 0; Mismatches 0; Indels
                                                                                                            ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 36,669
REFERENCE/DOCKET NUMBER: LUD 5611.1 JEL/MAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 74; DB 13; Best Local Similarity 100.0%; Pred. No. 8e-05; Matches 16; Conservative 0; Mismatches 0;
Fulbright & Jaworski L.L.P.
                                                                                                                                                                           COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/085,108
FILING DATE: 01-Mar-2002
CLASSIFICATION: <un>

UNKNOWN>

                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/501,104
FILING DATE: 09-Feb-2000
APPLICATION NUMBER: 09/468,433
FILING DATE: December 17, 1999
APPLICATION NUMBER: 09/066,281
FILING DATE: April 24, 1998
APPLICATION NUMBER: 08/845,528
FILING DATE: April 25, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 021505w0/JH/m1
CURRENT APPLICATION NUMBER: US/10/177,390
UNRENT FILING DATE: 2002-06-20
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PATENTIN Ver: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acids
STRANDEDNESS: single stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Mary Anne Schofield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                     STREET: 666 Fifth Avenue CITY: New York City STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (212) 3.18-3400
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                277 VKVLEYVIKVSARVRF 292
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Best Local Similarity 100.(
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-085-108-10
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US-10-177-390-18
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LENGTH: 309
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         APPLICANT: Stroobant, Vincent
APPLICANT: Stroobant, Vincent
APPLICANT: Demotte, Nathalie
APPLICANT: Demotte, Nathalie
APPLICANT: Schultz, Erwin
ITILE OF INVENTION: MAGE ANTIGENIC PEPTIDES WHICH BIND HLA-B35 AND HLA-B44
FILE REPERENCE: L0461/7104
CURRENT APPLICATION NUMBER: US/09/766,889A
CURRENT APPLICATION NUMBER: US 60/177,242
PRIOR FILING DATE: 2000-01-20
PRIOR FILING DATE: 2000-10-25
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FRASESQ for Windows Version 3.0
SEQ ID NO 2
SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 828, Application US/10296734

Publication No. US20040054137A1

GENERAL INPORMATION:

APPLICANT: Thompson, Scott A

TITLE OF INVENTION: Synthetic molecules and uses therefor

FILE REFERENCE: Savine

CURRENT APPLICATION NUMBER: US/10/296,734

PRIOR APPLICATION NUMBER: US/10/296,734

PRIOR APPLICATION NUMBER: AU PQ7761/00

PRIOR FILING DATE: 2000-05-26

NUMBER OF SEQ ID NOS: 1507

SOFTWARE: Patentin version 3.2

SEQ ID NO 828

LENGTH: 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 74; DB 9; Length 309;
Pred. No. 8e-05;
); Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-296-734-828
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                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
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Publication No. US20040180058A1;
GENERAL INFORMATION:
APPLICANT: Sharman. M.
TITLE OF INVENTION: Vaccine Compositions and Methods;
FILE REFERENCE: 25955-003;
CURRENT FILING DATE: 2003-12-19
PRIOR APPLICATION NUMBER: 60/435,500
PRIOR RILING DATE: 2002-12-20;
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
CURRENT APPLICATION NUMBER: US/10/117,937
CURRENT FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: US 60/202,211
PRIOR FILING DATE: 2001-04-06
PRIOR FILING DATE: 2001-10-07
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 602
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 71
LENGTH: 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 71, Application US/10657022
Publication No. US20040180354A1
GENERAL INPORMATION:
APPLICANT: Simard, John J. L.
APPLICANT: Diamond, David C.
APPLICANT: Liu, Liphing
ITILE OF INVENTION: EPITOPE SEQUENCES
FILE REFERENCE: MANNK.032A
CURRENT APPLICATION NUMBER: US/10/657,022
CURRENT APPLICATION NUMBER: 60/409123
PRIOR RILING DATE: 2003-09-06
NUMBER OF SEQ ID NOS: 610
SOFTWARE: FRRESCO FOR Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              277 VKVLEYVIKVSARVRF 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VKVLEYVIKVSARVRF 16
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Best Local Similarity 100.0
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US-10-657-022-71
                                                                                                                                                                                                                                                                                                                                                  US-10-117-937-71
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US-10-741-466-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
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                                                                                                                                                                  Sequence 10, Application US/10160237
Publication No. US20030170256A1
GENERAL INFORMATION:
APPLICANT: LUCAS, Sophie; DE SMET, Charles; BOON-FALLEUR, Thierry
APPLICANT: LUCAS, Sophie; DE SMET, Charles; BOON-FALLEUR, Thierry
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE CODING
FOR TUMOR REJECTION ANTIGEN PRECURSOR MAGE-C1 AND MAGE-C2
AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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100.0%; Score 74; DB 14; Length 309;
Best Local Similarity 100.0%; Pred. No. 8e-05;
Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage medium Type: Diskette, 3.5 inch, 360 kb storage medium Type: Diskette, 3.5 inch, 360 kb storage software: IBM PS/2 OPERATING SYSTEM: PC-DOS SOFTWARE: Wordperfect CURRIT APPLICATION NUMBER: US/10/160,237

FILING DATE: 04-Jun-2002

CLASSIFICATION: -UNKnown>
PRIOR APPLICATION: -UNKnown>
PRIOR APPLICATION: -UNKnown>
PRIOR APPLICATION: -UNKnown>
PRIOR APPLICATION: -UNKnown>
FILING DATE: April 24, 1998

APPLICATION NUMBER: US/09/066,2818

FILING DATE: April 24, 1998

APPLICATION NUMBER: 08/845,528

FILING DATE: April 25, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - JEL/MAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Mary Anne Schofield
REGIETRATION NUMBER: 36,669
REFERENCE/DOCKET NUMBER: LUD 5455.2 US
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 20
CORRESSONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 10: US-10-160-237-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acids
STRANDEDNESS: single stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 71, Application US/10117937
Publication No. US20030220239A1
GENERAL INFORMATION:
APPLICANT: CTL INMUNO THERAPIES CORP.
APPLICANT: SIMARD, John, J.L.
APPLICANT: LIV, Liping
APPLICANT: LIV, Liping
APPLICANT: XIE, Zhidong
TITLE OF INVENTION: EPITOPE SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (212) 318-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                     277 VKVLEYVIKVSARVRF 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 VKVLEYVIKVSARVRF 16
          1 VKVLEYVIKVSARVRF
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RESULT 14
US-10-164-078A-32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 74; DB 16; Length 311; Best Local Similarity 100.0%; Pred. No. 8.1e-05; Matches 16; Conservative 0; Mismatches 0; Indels (
                                                                                                                               Query Match 100.0%; Score 74; DB 16; Length 309; Best Local Similarity 100.0%; Pred. No. 8e-05; Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:

APPLICANT: Sherman, M.

APPLICANT: Sherman, M.

TITLE OF INVENTION: Vaccine Compositions and Methods
FILE REFERENCE: 25955-003

CURRENT FILING DATE: 2003-12-19

PRIOR FILING DATE: 2002-12-20

PRIOR FILING DATE: 2002-12-20

PRIOR FILING DATE: 2002-12-20

PRIOR FILING DATE: 2002-12-20

NUMBER OF SEQ ID NOS: 8

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 8

LENGTH: 311
                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/10741466

Publication No. US20040180058A1

GENERAL INFORMATION:

APPLICANT: Sherman, M.

APPLICANT: Sherman, M.

APPLICANT: Sherman, M.

TITLE OF INVENTION: Vaccine Compositions and Methods

FILE REFERENCE: 25955-003

CURRENT APPLICATION NUMBER: US/10/741,466

CURRENT FILING DATE: 2003-12-19

PRIOR FILING DATE: 2002-12-0

NUMBER OF SEQ ID NOS: 8

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 7
                                                                                                                                                                                                                                              277 VKVLEYVIKVSARVRF 292
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                                                                                                                                                                                                                   1 VKVLEYVIKVSARVRF 16
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; ORGANISM: Influenza A virus
US-10-741-466-7
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; ORGANISM: Influenza A virus
US-10-741-466-8
                                      TYPE: PRT
ORGANISM: Influenza A virus
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US-10-741-466-8
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SEQ ID NO 6
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279 VKVLEYVIKVSARVRF 294

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US-10-164-121A-33

Sequence 33, Application US/10164121A

Publication No. US2030228308A1

GENERAL INFORMATION:

APPLICANT: Zhang, Yi

APPLICANT: Boon, Thierry

APPLICANT: Van der Bruggen, Pierre

APPLICANT: Traversari, Catra

TITLE OF INVENTION: Isolated Peptides Which Bind to HLA-Cw6 Molecules And Uses Therec

FILE REFERENCE: LUD-5771

CURRENT APPLICATION UNDBER: US/10/164,121A

CURRENT APPLICATION UNDBER: US/10/164,121A
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Sequence 1454, Application US/10296734

Publication No. US20040054137A1

GENERAL INFORMATION:

APPLICANT: Thompson, Scott A

TITLE OF INVENTION: Synthetic molecules and uses therefor

FILE REFERENCE: Savine

CURRENT APPLICATION NUMBER: US/10/296,734

CURRENT FILING DATE: 2003.08-04

PRIOR FILING DATE: 2000-05-26

NUMBER OF SEQ ID NOS: 1507

SEQ ID NO 1454

LENGTH: 3541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77.0%; Score 57; DB 15; Length 12; 100.0%; Pred. No. 0.0024; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Melanoma cancer specific savine US-10-296-734-1454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
100.0%; Score 74; DB 12;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 16; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 32, Application US/10164078A; Publication No. US20030228325A1; GENERAL INFORMATION:
APPLICANT: Bilaborough, Janine; APPLICANT: Schultz, Erwin APPLICANT: Van der Bruggen, Pierre; APPLICANT: Van der Bruggen, Pierre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1700 VKVLEYVIKVSARVRF 1715
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: H. sapiens
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APPLICANT: Boon, Thierry

TITLE OF INVENTION: Isolated Peptides Which Bind to HLA-B18 Molecules And Uses Thereo FILE REPERENCE: LUD-5756

CURRENT APPLICATION NUMBER: US/10/164,078A

CURRENT FILING DATE: 2002-06-05

NUMBER OF SEQ ID NOS: 35

LENGTH: 12
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Sequence 2, Application US/10218095
Publication No. US20040033541A1
GENERAL INFORMATION:
APPLICANT: Zhang, Yi
APPLICANT: Stroobant, Vincent
APPLICANT: Buseo, Vincent
APPLICANT: Waso, Vincent
APPLICANT: Waso, Vincent
APPLICANT: Was der Bruggen, Pierre
ITILE OF INVENTION: MAGE-A4 ANTIGENIC PEPTIDES AND USES THEREOF
FILE REFERENCE: LOO461/70137
CURRENT APPLICATION NUMBER: US/10/218,095
CURRENT FILING DATE: 2002-08-13
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn version 3.1
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                                                                                                                                                                                                                                                                                                                   Query Match 77.0%; Score 57; DB 15; Length 12; Best Local Similarity 100.0%; Pred. No. 0.0024; Matches 12; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                    TYPE: PRT
ORGANISM: H. sapiens
                                                                                                                                                                                                                                                          ; FEATURE:
US-10-164-078A-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 2
LENGTH: 317
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Search completed: October 7, 2004, 15:33:46 Job time : 60.6364 secs

285 VKVLEHVVRVNARVR 299

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33, Appl 7428, Ap 23030, Ap 26, Appl 31, Appl 11, Appl 11, Appl 602, Appl 70, Appl 71, Appl 7

Sequence 3 Sequence 4 Sequence 6

Sequence 2 Sequence 2 Sequence 2 Sequence 2 Sequence 3 Sequence 4 Sequence 6 Sequence 6 Sequence 6

Sequence Sequence Sequence

4

Title: Perfect score:

Sequence:

Searched:

OM protein

Run on:

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Query Match 100.0%; Score 74; DB 1; Length 58; Best Local Similarity 100.0%; Pred. No. 6e-06; Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Files, John D.
APPLICANT: Files, John D.
APPLICANT: Sette, Alessandro D.
APPLICANT: State, Alessandro D.
APPLICANT: State, Alessandro D.
APPLICANT: State, Alessandro D.
APPLICANT: State, Alessandro D.
TITLE OF INVENTION: IMMUNOGENIC PEPTIDES (as amended)
NUMBER OF SEQUENCES:
TYPLE OF SEQUENCES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STRATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/465,167A
FILING DATE: 05-JUN-1995
CLASSIFICATION NUMBER: US 08/103,623
FILING DATE: 06-JUS-1995
APPLICATION NUMBER: US 08/103,623
APPLICATION NUMBER: 13/90
REFERENCE/DOCKET NUMBER: 14/137-60-1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                  PCT-US95-02121-152
US-09-328-357-5371
US-08-45-328-357-7428
US-09-328-357-7428
US-09-328-357-7428
US-09-328-357-7428
US-09-340-236-3375
US-09-465-167A-31
US-08-465-167A-17
US-08-465-167A-46
US-08-465-167A-46
US-08-465-167A-17
US-08-657-820-17
US-09-698-41
US-09-698-41
US-09-049-915A-6
US-08-005-002C-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIF: 98111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 1, Application US/08465167A; Patent No. 5750395; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
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917
1264
1264
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
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                                                                                                                                                              October 7, 2004, 15:18:26; Search time 17.4545 Seconds (without alignments) 47.324 Million cell updates/sec
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/cgn2_6/ptodata/2/jaa/BECOMB.pep:*
/cgn2_6/ptodata/2/jaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/jaa/PCTUS_COMB.pep:*
                          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-627-820-1

US-08-945-167A-24

US-08-943-118-10

US-08-845-528C-10

US-09-392-114-29

US-09-392-114-29

US-09-392-114-29

US-09-392-114-29

US-08-465-167A-15

US-08-465-167A-15

US-08-465-167A-44

US-08-465-167A-44

US-08-465-167A-44

US-08-465-167A-39

US-08-465-167A-44

US-08-465-167A-39

US-08-465-167A-39

US-08-465-167A-39

US-08-465-167A-39

US-08-465-167A-39

US-08-465-167A-27

US-08-197-448-152

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US-08-197-448-152

US-08-197-484-152

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US-08-197-484-152
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                         - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                          US-09-336-091-3
74
1 VKVLEYVIKVSARVRF 16
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Maximum DB seq length: 200000000
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Match Length
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Score

Result Š. ö

Gaps

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Sequence 10, Application US/08993118

Patent No. 5997872

GENERAL INFORMATION:
APPLICANT: LUCAS, Sophie;
APPLICANT: BOON-FALLEUR, Thierry
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE CODING FOR TUMOR
TITLE OF INVENTION: REJECTION ANTIGEN PRECURSOR MAGE-C1 AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 74; DB 1; Length 309; 100.0%; Pred. No. 3.5e-05; ive 0; Mismatches 0; Indels
TITLE OF INVENTION: IMMUNOGENIC PEPTIDES (as amended)
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
                                                                                                                                                                                                           COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,167A
FLING DATE: 05-JUN-1995
PROR APPLICATION NUMBER: US/08/465,167A
FLING DATE: 06-JUN-1995
PRICKALTION NUMBER: US/08/103,623
FILING DATE: 06-AUG-1993
ATYORNEY/AGENT INFORMATION:
NAME: Patmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 31,990
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: AUTHOR
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COMPUTER READABLE FORM:
MEDIUM TYPE: _________________A.5 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDERfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,118
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       277 VKVLEYVIKVSARVRF 292
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3T: 805 Third Avenue
: New York City
3: New York
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Best Local Similarity 100.
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US-08-993-118-10
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                                                                                                                                                                                                                                                            APPLICANT: Fikes, John D.
Livingston, Brian D.
Sette, Alessandro D.
Sidney, John C.
Sidney, John C.
TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTY: U.S.A.

ZIR: 94105

COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: 1BM PC Compatible
COMPUTER: 1BM PC Compatible
COMPUTER: 1BM PC Compatible
COMPUTER: 1BM PC COMPA: 100 MB-1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627, 820
FILING DATE: 02-Apr-1996
CLASSIFTCATION: Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/103,623
FILING DATE: cUnknown>
ATTORNEY/AGENT INFORMATION:
NAME: PEATMELE, SLEVEN W.
REGISTRATION NUMBER: 31,990
REFERENCE/COCKET NUMBER: 14137-60
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Tower
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100.0%; Score 74; DB 4; Length 58;
Best Local Similarity 100.0%; Pred. No. 6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels
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APPLICANT: Livingston, Brian D.
APPLICANT: Sette, Alessandro D.
APPLICANT: Sidney, John C.
TITLE OF INVENTION: DNA ENCODING MAGE-1 C-TERMINAL
                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie
STREET: One Market Plaza, Steuart Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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                                                                                                                                                                                        Sequence 1, Application US/08627820 Patent No. 6464980 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
                                                       26 VKVLEYVIKVSARVRF 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: San Francisco
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                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
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APPLICANT: Fikes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 3
US-08-465-167A-24
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Gaps

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Sophie; DE SMET, Charles; BOON-FALLEUR, Thierry
1: ISOLATED NUCLEIC ACID MOLECULE CODING
1: FOR TUNOR RELECTION ANTIGEN PRECURSOR MAGE-C1 AND MAGE-C2
1: AND USES THEREOF
  Gaps
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Sequence 24, Application US/08627820
Settent No. 6464980
GENERAL INFORMATION.
Livingston, Brian D.
Sette, Alessandro D.
Sidney, John C.
TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 74; DB 4; Length 309;
100.0%; Pred. No. 3.5e-05;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Street Tower
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYBE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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Mismatches
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APPLICATION NUMBER: US/08/103,623
FILING DATE: cUNKNOWN:
ATTORNEY/AGENT INFORMATION:
NAME: PARTABLES, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/627,820
FILING DATE: 02-Apr-1996
CLASSIFICATION: <UNKNOWN>
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-08-627-820-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (206) 467-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION
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                                                                                  277 VKVLEYVIKVSARVRF 292
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INFORMATION FOR SEQ ID NO: 24:
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                                               1 VKVLEYVIKVSARVRF
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Best Local Similarity 100.0
....hes 16; Conservative
  16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.
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  Matches
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APPLICANT: LUCAS, Sophie;
APPLICANT: LUCAS, Sophie;
APPLICANT: DE SNET, Charles;
APPLICANT: BEON-FALLEUR, Thierry
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE CODING FOR TUMOR TITLE OF INVENTION: THEREOF NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STRET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
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ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage COMPUTER: IBM FS/2
OPERATING SYSTEM: PC-DOS
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,528C
FILING DATE: April 25, 1997
CLASSIFICATION: 4335
ATTOMICATION NUMBER: 156,669
REGISTRATION NUMBER: 156,669
REGISTRATION NUMBER: 156,669
REGISTRATION NUMBER: 156,669
REGISTRATION NUMBER: 150,669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/645,528
FILING DATE: APril 25, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mary Anne Schofield
REGISTATION NUMBER: 15, 669
REFERENCE/DOCKET NUMBER: 14D 5455
TELECOMMUNICATION INFORMATION:
TELEFHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Application US/08845528C Patent No. 6027924 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                   SS: single stranded
linear
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Best Local Similarity 100.0
Matches 16; Conservative
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STRANDEDNESS: sinc
                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acids
STRANDEDNESS: sing
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Best Local Similarity
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                              309
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Sequence 15, Application US/08465167A
Patent No. 5750395
GENERAL INFORMATION:
APPLICANT: Fixes, John D.
APPLICANT: Sette, Alessandro D.
APPLICANT: Sidney, John C.
APPLICANT: Sidney, John C.
TITLE OF INVENTION: IMMUNOGENIC PEPTIDES (as amended)
NUMBER OF SEQUENCES: 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 74; DB 4; L
Best Local Similarity 100.0%; Pred. No. 3.5e-05;
Matches 16; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 3.5e-05;
tive 0; Mismatches 0;
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/845,528
FILING DATE: APPLICATION
NUMBER: 08/845,528
ATTORNS/AGENT INFORMATION:
NAME: Mary Anne Schofield
REGISTRATION NUMBER: 36,669
REFERENCE/DOCKET NUMBER: LUD 5611 JEL/WAS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 662-0200
TELEPHONE: (202) 662-4643
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
LENGTH: 309
                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acids
STRANDEDNESS: single stranded
TOPOLOGY: linear
US-09-468-433C-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 277 VKVLEYVIKVSARVRF 292
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Best Local Similarity 100.
Matches 16; Conservative
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US-09-392-714-29
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US-08-465-167A-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Wordporfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/066,281B
FILING DATE: April 24, 1998
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/845,528
FILING DATE: April 25, 1997
ATTORNEY/AGENT INFORMATION:
NAME: MAY Anne Schoffeld
REGISTRATION NUMBER: 15,669
REGISTRATION NUMBER: LUD 5455.2 US - JEL/MAS
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: (212) 318-3100
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10103
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OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/468,433C
FILING DATE: December 17, 1999
CLASSFICATION:
PRIOR APPLICATION DATA:
APPLICATION D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acids
STRANDEDNESS: single stranded
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            277 VKVLEYVIKVSARVRF 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 VKVLEYVIKVSARVRF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0
Matches 16; Conservative
     NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-066-281B-10
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100.0%; Pred. No. 0.067;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 595, Application US/08159339A
Fatent No. 6037135
GENERAL INFORMATION:
APPLICANT: Kubo, Ralph T.
APPLICANT: Sette, Alessandro
APPLICANT: Sette, Alessandro
TITLE OF INVENTION: HLA Binding peptides and Their
TITLE OF INVENTION: Uses
NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
ADDRESSED: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Bighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTRY: USA
ZIP: 94111-3834
COMPUTRY: USA
COMPUTRY READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: DISKETCH
COMPUT
         US 08/103,623
                             FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: PARTMELE, SICHON,
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: '10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-465-167A-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 LEYVIKVSAR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 LEYVIKVSAR 10
         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-159-339A-595
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i Sequence 49, Application US/08465167A

i Patent No. 5753395

i GENERAL INPERMATION:

APPLICANT: Fikes, John D.

APPLICANT: Sette, Alessandro D.

APPLICANT: Sitney, John C.

ITLE OF INVENTION: IMMUNOGENIC PEPTIDES (as amended)

INTEREPT: TOPENSES:

APPLICANT: SEQUENCES: SITURE OF INVENTION: IMMUNOGENIC PEPTIDES (as amended)

INTEREPT: TOPENSES:

CORRESPONDENCES: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 62.2%; Score 46; DB 1; Length 10; Best Local Similarity 100.0%; Pred. No. 0.067; Matches 10; Conservative 0; Mismatches 0; Indels
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ZIP: 98111
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,167A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/103,623
FILING DATE: 06-A0C-1993
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-60-1
TELEPHONE: 206-467-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14137-60-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 10 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-08-465-167A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 YVIKVSARVR 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CA
USA
                                                                                                                                                            USA
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                                                                                           CITY: San F
STATE: CA
COUNTRY: US
ZIP: 98111
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US-08-465-167A-4
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TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF THE COMPLETE MAGE 1 GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPES: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/NS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/627,820

FLING DATE: 02-Apr-1996

CLASSIFICATION NUMBER: US/08/103,623

FLING DATE: CUNROWN-

APPLICATION NUMBER: US/08/103,623

FLING DATE: CUNROWN-

ATTORNEY PARTELES (100)

REGISTRATION NUMBER: 14137-60

TELEBHONE: (206) 467-9600

TELEBHONE: CAPARTERISTICS:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Street Tower CITY: San Francisco
                                                                                                                             Query Match 62.2%; Score 46; DB 3; Length 10; Best Local Similarity 100.0%; Pred. No. 0.067; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62.2%; Score 46; DB 4; Length 10; 100.0%; Pred. No. 0.067; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Fikes, John D.
Livingston, Brian D.
Sette, Alessandro D.
                                                                                                                                                                                                                                                                                                                                                                        Sequence 15, Application US/08627820
Patent No. 6464980
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0
Matches 10, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U.S.A.
           STRANDEDESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-159-339A-595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 YVIKVSARVR 10
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TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                        US-08-627-820-15
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RESULT 14

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; Sequence 4, Application US/08465167A
; Patent No. 5750395
; GENERAL INFORMATION:
    APPLICANT: Fikes, John D.
    APPLICANT: Fikes, John D.
    APPLICANT: Sette, Alessandro D.
    APPLICANT: Sidney, John C.
    TITLE OF INVENTION: DNA ENCODING MAGE-1 C-TERMINAL
    TITLE OF INVENTION: INMUNOGENIC PEPTIDES (as amended)
    NUMBER OF SEQUENCES: 51
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Townsend and Townsend and Crew LIP
    STREET: Two Embarcadero Center, 8th Floor
    CITY: San Francisco
                                                                      APPLICANT: Fixes, John D.
APPLICANT: Sette, John D.
APPLICANT: Sette, Alessandro D.
APPLICANT: Sette, John C.
TITLE OF INVENTION: DNA ENCODING MAGE-1 C-TERMINAL
TITLE OF INVENTION: IMMUNOGENIC PEPTIDES (as amended)
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,167A
FILING DATE: 05-UNN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 45; DB 1; Ler
; Pred. No. 0.099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/103,623
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 98111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS_DOS
; Sequence 39, Application US/08465167A; Patent No. 5750395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 60.8%; Scc
Best Local Similarity 100.0%; Pi
Matches 10; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEPAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VLEYVIKVSA 10
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                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: C.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,167A
FILING DATE: 05-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/103,623
FILING DATE: 06-MUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-60-1
TELEPHONE: 206-467-9600
INFORMATION FOR EQUINO: TELEFAX: 415-576-0300
INFORMATION OF REQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-465-167A-4
```

Search completed: October 7, 2004, 15:19:25 Job time : 18.4545 secs

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein October 7, 2004, 15:17:11; Search time 18.5455 Seconds (without alignments) 82.989 Million cell updates/sec Run on:

US-09-336-091-3 74 1 VKVLEYVIKVSARVRF 16 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched: Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB 8 Maximum DB 8

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 sm

Database :

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		& Query			SUMMAKIES	
Score	:	Match	Length	BB	·	Description
26		75.7	317	7	138661	melanoma antigen M
40		54.1	242	~	D72218	conserved hypothet
40		54.1	542	7	E86628	prophage psi prote
40		54.1	594	0	F72265	hyp
39		52.7	379	7	T04645	hypothetical prote
39		52.7	444	N	H82992	aminopeptidase P P
39		52.7	530	0	D70476	DNA helicase - Aqu
38.5		52.0	341	N	F90084	hypothetical prote
38		51.4	357	N	H71122	
38		51.4	390	7	T10231	44
38		51.4	493	7	H70479	leucine aminopepti
38		51.4	761	~	D70447	tetrahydropteroylt
38		51.4	846	N	H70871	hypothetical prote
38		51.4		7	A86983	
38		51.4		7	S72760	ppsl protein - Myc
37.5		50.7		~	G96813	hypothetical prote
37		50.0		~	E90331	hypothetical prote
37		50.0		~	C70114	ribosomal protein
37		50.0		~	C96540	hypothetical prote
37		50.0		N	A97145	ABC-type iron (III
37		50.0		N	F69758	transcription regu
37		50.0		0	D90166	hypothetical prote
37		50.0	407	7	D86973	probable chorismat
37		50.0	543	0	G83825 .	hypothetical prote
37		50.0	544	N	S54531	
37		50.0	664	7	B81269	
37		50.0	946	0	T01460	
37		50.0	1070	-	A54600	1-phosphatidylinos
37		50.0	1253	~	F86436	hypothetical prote

A;Molecule type: mRNA A;Residues: 1-172, TT',174-306,'Q',308-317 <DIN> A;Cross-references: EMBL:U10340; NID:g499123; PIDN:AAA19007.1; PID:g499124 A;Experimental source: melanoma cell line DMI50

A; Accession: JC2359

C,Superfamily: tumor associated protein MAGE F,169-177/Region: HLA-A1 binding #status predicted

A, Molecule type: DNA A, Residues: 169-172, '7', 174-177 < TRA2> A, Experimental source: antigen MAGE-41 R; Ding, M.; Beck, R.J.; Keller, C.J.; Fenton, R.G. Blochem Blophys. Res. Commun. 202, 549-555, 1994 A;Title: Cloning and analysis of MAGE-1-related genes. A, Reference number: JC2358; MUID:94311935; PMID:8037761

A;Molecule type: DNA A;Residues: 169-177 <TRA1> A;Experimental source: antigen MAGE-4

A; Accession: PH1298

hypothetical prote fatty-acid synthas	collagen alpha 1(V hypothetical prote	hypothetical prote hypothetical prote	unknown protein Ti	melanoma antigen M	holliday junction	beca-N-acetyinexos hypothetical prote	. coenzyme PQQ synth	coenzyme PQQ synth	hypothetical prote	glycosyltransferas
C84507 S61703	A54849 T33346	T17491 B72764	A96664	JC2360	AH3293	A1338/ T24822	F90323	D90347	S72753	AB2456
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1738	2944 646	159	200	314	346	355	378	378	392	429
50.0	50.0	48.6	48.6	48.6	48.6	48.6	48.6	48.6	48.6	48.6
37 37	37 36.5	36	36	36	36	36	36	36	36	36
30 31	32 33	3.4	36	38	99	41	42	43	44	45

## ALIGNMENTS

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C;Species: Homo sapiens (man)
C;Date: 07-Jun-1996 #sequence revision 07-Jun-1996 #text change 18-Feb-2000
C;Accession: I38661; I38662; PH1297; PH1298; JC2359; G01446
R;De Plaen, E.; Arden, K.; Traversari, C.; Gaforio, J.J.; Szikora, J.P.; De Smet, C.; Boon, T.
                                                                                                                                                                                                                                                                                                                                                    the MAGE fa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:U10688; NID:9533516; PIDN:AAA68872.1; PID:9533517
A;Experimental source: antigen MAGE-4b
B;Txaversari, C.; van der Bruggen, P.; Luescher, I.F.; Lurquin, C.; Chomez, P.; Van Pel
J: Exp. Med. 176, 1453-1457, 1992
A;Title: A nonapeptide encoded by human gene MAGE-1 is recognized on HLA-A1 by cytolyti
A;Reference number: PH1294; MUID:93018875; PMID:1402688
                                                                                                                                                                                                                                                                                                  Immunogenetics 40, 360-369, 1994
A;Title: Structure, chromosomal localization, and expression of 12 genes of
A;Reference number: 138659; MUID:95012457; PMID:7927540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Residues: 1-317 <DEP1>
A,Residues: 1-317 <DEP1>
A,Cross-references: EMBL:U10687; NID:g533514; PIDN:AAA68871.1; PID:g533515
A,Experimental source: antigen MAGE-4a
melanoma antigen MAGE-4 - human
N;Alternate names: MAGE 41 protein; melanoma antigen MAGE-X2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: 138662
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-172,'T',174-317 <DEP2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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C;Accession: F72265
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
                                                                                                                  Nature 399, 323-329, 1999
Affille: Evidence for lateral gene transfer between Archaea and Bacteria from genome sec
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: F72265
                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-594 <ARN>
A; Residues: 1-594 <ARN>
A; Cross-references: GB:AE001788; GB:AE000512; NID:g4981893; PIDN:AAD36406.1; PID:g498185
A; Experimental source: strain MSB8
C; Genetics:
A; Gene: TM1334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein F10N7.190 - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (Species: Arabidopsis thaliana (mouse-ear cress) (Spacies: 3-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Sep-1999 (Spacession: T04645 #sequence_revision 23-Apr-1999 #text_change 20-Sep-1999 (Spacession: T04645 #submitted to the Protein Sequence Database, March 1999 Apreference number: Z15263 Apreference number: Z15263 Apreference number: Z15263 Apreference number: Z15263 Apreferences: EMBL:ALO21636 Apresidues: 1-379 < EMBL:ALO21636 Apresimental source: cultivar Columbia; BAC clone F10N7 (Specifics)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: H82992
R;Stover, CK.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Badman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Nature 406, 959-964, 2000
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathx A;Reference number: A82950; MUID:20437337; PMID:10984043
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A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-444 <STO>
A; Cross-references: GB: AE004935; GB: AE004091; NID: G9951526; PIDN: AAG08609.1; GSPDB: GN003
A; Experimental source: strain PAO1
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A;Introns: 48/1; 221/1; 252/3; 287/1; 326/3
A;Note: F10N7.190
C;Superfamily: kinase-related transforming protein; protein kinase homology
11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
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Pred. No. 29;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                         Score 40; DB 2;
Pred. No. 30;
1; Mismatches
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illarity 66.7%;
Conservative
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288 LEYIIKKGGRVR 299
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14 VSVLEFIISVSA 25
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Best Local Similarity
Matches 8; Conserv
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Best Local Similarity
Matches 8; Conserv
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A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: D72218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Cross-references: GB:AE001812; GB:AE000512; NID:g4982302; PIDN:AAD36806.1; PID:g498231
A,Experimental source: strain MSB8
Genetic Conserved hypothetical protein H10860
                                                                                                                                                                                                                                                                                                                                                       C;Accession: D72218
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
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A;Experimental source: strain ILL403
C;Genetics:
                                                                                                                                                                                                                                                                                 conserved hypothetical protein - Thermotoga maritima (strain MSB8)
C,Species: Thermotoga maritima
C,Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
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C;Species: Thermotoga maritima
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                   Length 317;
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                      DB 2;
0.018;
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Pred. No. 27;
4; Mismatches
                                                                   4; Mismatches
                   75.7%; Score 56; 73.3%; Pred. No.
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127 VKVTETVVKVSAGTVF 142
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                 Query Match
Best Local Similarity 73.34
Matches 11, Conservative
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A;Molecule type: DNA
A;Residues: 1-242 <ARN>
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Best Local Similarity
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 392, 353-358, 1998
A,Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A,Reference number: A70300; MUID:98196666; PMID:9537320
A,Accession: H70479
A,Status: preliminary; nucleic acid sequence not shown; translation not shown
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C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 03-Mar-2003
C;Accession: H70479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: PH0751
C;Superfamily: Archaeoglobus fulgidus conserved hypothetical protein AF1032
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A;Experimental source: cultivar Columbia; BAC clone F11111
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 38; DB 2; Length 357;
Pred. No. 42;
2; Mismatches 2; Indels
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                                                                                - Pyrococcus horikoshii
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Pred. No. 46;
4; Mismatches
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llarity 53.3%;
Conservative '
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| | | | | | | ::: | :| |
345 VYVLEYMLEESKKVR 359
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Best Local Similarity 52.4%;
Matches 11; Conservative
                                                                                hypothetical protein PH0751
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Best Local Similarity
8; Conserva
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A; Residues: 1-390 <BEV>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Map position: 4
A; Introns: 60/1; 249/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
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A;Experimental source: strain VF5
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein orf341 [imported] - Guillardia theta nucleomorph (5.5pecies: nucleomorph Guillardia theta (5.5pecies: nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont (5.5pecies: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001 (5.5Accession: F90084 (8.5 Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Rei Nature 410, 1091-1096, 2001 (8.5 Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Rei A; Title: The highly reduced genome of an englaved algal nucleus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
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A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: D70476
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A;Molecule type: DNA
A;Residues: 1-341 < DOU's
A;Cross-references: GB:AF165818; NID:g13794434; PIDN:AAK39809.1; GSPDB:GN00150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;Species: Aquifex aeolicus
;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
;Accession: D70476
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                                                                                                                                                                         Length 444;
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%
                                                                                                                                                                    DB 2;
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Pred. No. 41;
5; Mismatches
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44.4%; Pred. No. 32;
ive 5; Mismatches
                                                                                                                                                                    Score 39; DB
Pred. No. 34;
2; Mismatches
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162 IKILEYLIIPHKLKKRIR 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 VKVLEYVI---KVSARVR 15
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                                                                                                                                                                Query Match 52.7%;
Best Local Similarity 61.5%;
Matches 8; Conservative
                                   A;Gene: pepP; PA5224
C;Superfamily: aminopeptidase P
                                                                                                                                                                                                                                                                                                                                                                                                                         181 VKVMRYAAEVSAR 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA helicase - Aquifex aeolicus
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412 VKIVEYLMKIGLR 424
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Best Local Similarity 44.4
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                         1 VKVLEYVIKVSAR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 46.2
Matches 6; Conservative
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Nature 392, 353-358, 1998
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A;Genome: nucleomorph
C;Keywords: nucleomorph
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C;Genetics:
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Association 19

Conserved hypothetical protein ML0593 [imported] - Mycobacterium leprae

Cispeciaes: Ridera, Riselameier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho

R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,

Cam, M.A.; Rutherford, K.M.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Su

A; Althors: Ruther, S.; Seegar, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Su

A; Althors: Ruther, S.; Seegar, M.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Su

A; Reference number: A86993

A; Reference number: A86993

A; Retsidues: 1-869 <STO>

A; Residues: 1-869 <STO>
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A;Residues: 202-481,'A',483-589 <PAR>
A;Cross-references: EMBL:299125; NID:g2398683; PIDN:CAB16172.1; PID:e343548; PID:g239870
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pps1 protein - Mycobacterium leprae
N;Alternate names: B1496_C2_189 protein
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 23-Mar-2001
C;Accession: S72760; T1013
R;Smith, D.R.; Robison, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-869 <SMI>
A;Cross-references: EMBL:U00013; NID:g466868; PIDN:AAA17127.1; PID:g466882
R;Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, September 1997
A;Reference number: Z16918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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nilarity 50.0%; Pred. No. 1e+02;
Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 38; DB 2;
Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, November 1993
A; Description: Mycobacterium leprae cosmid B1496.
A; Reference number: S72695
A; Accession: S72760
A; Status: preliminary
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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Job time: 21.5455 secs
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                               |:| ::| ||||:
626 VVEIIVKPHARVRY 639
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649 VVEIIVKPHARVRY 662
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649 VVEIIVKPHARVRY 662
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Best Local Similarity 50.0%
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nes 7; Conserv
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                                               g
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C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: H70871
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Comor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: A70500; MUD:98295987; PMID:9634230
A;Accession: H70871
A;Accession: H70871
A;Reference number: A70500; MUD:98295987; PMID:9634230
A;Accession: H70871
A;Residues: 1-846 <COL>
A;Coss-references: GB:AL021184; GB:AL123456; NID:93261498; PIDN:CAA15991.1; PID:e123745
A;Genetics:
A;Genetics: A;Genetics: Strain H37RV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Varure 392, 353-358, 1998

A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-761 <AQF>
A;Cross-references: GB:AE000752; NID:92984021; PIDN:AAC07565.1; PID:92984022; GB:AE00065
C;Genetics:
A;Cross-references: strain VFS
C;Genetics:
A;Genetics:
A;Genetics:
C;Superfamily: cobalamin-independent methionine synthase
               A Residues: 1-493 <AQF>
A; Residues: 1-493 <AQF>
A; Cross-references: GB:AE000772; NID:g2984299; PIDN:AAC07829.1; PID:g2984306; GB:AE00065
A; Experimental source: strain VF5
C; Genetics: A; Gene: pepA
C; Superfamily: Cytosol aminopeptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tetrahydropteroyltriglutamate methyltransferase - Aquifex aeolicus
C.Species: Aquifex aeolicus
C.Date: O8-May-1998 #sequence_revision O8-May-1998 #text_change 18-Jun-1999
C.Accession: D70447
R.Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Oy
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57.1%; Pred. No. 90;
cive 4; Mismatches 2; Indels
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 [5]
MUTAGENESIS
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Compugen Ltd.
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             GenCore version (c) 1993 - 2004
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UBP2_YEAST
YKB4_YEAST
DOC2_MOUSE
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MAG4 HUMAN
MAG4 HUMAN
RPOC BENDE
TRU1 THETN
AMPA AQUAE
WETE AQUAE
NEE1 MYCLU
YE61 MYCLU
YE61 MYCLU
YE61 MYCLU
YE61 MYCLU
YE61 MYCLU
YE61 HUMAN
FRAC FUSINI
SAD FSESM
P11B HUMAN
FRAC TEMAN
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CA17 HUMAN
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SECUENCE FROM N.A. MEDLINES-2006661; PubMed=1840703; MEDLINES-2006661; PubMed=1840703; van der Bruggen P., Traversari C., Chomez P., Lurquin C., de Plaen B. van den Eynde B., Knuth A., Boon T.; handen encoding an antigen recognized by cytolytic T lymphocytes on a human melanoma."; Science 254:1643-1647(1991).
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MEDLINE=94157413; PubMed=8113684;
Gaugler B., van den Brude B., van der Bruggen P., Romero P.,
Gaforio J.J., de Plaen B., Lethe B., Brasseur F., Boon T.;
"Human gene MAGE-3 codes for an antigen recognized on a melanoma by autologous cytolytic T lymphocytes.";
J. Exp. Med. 179:921-930(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAGI HUMAN STANDARD; PRT; 309 AA.
P43355; 000346;
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Melanoma-associated antigen 1 (MAGE-1 antigen) (Antigen MZ2-E)
                       009203
P07752
Q8r7b9
Q58750
Q88nj4
Q06218
Q98ch0
Q91014
Q9vv73
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Chen H., Wang L., Mei M., Qin L., Cong X., Xu J., Wei L.,
Chen W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The polymorphism of MAGE-1 gene in Chinese people."; Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Skin, MEDLINE=94311935; PubMed=8037761; MEDLINE=94311935; PubMed=8037761; Back R.J., Keller C.J., Fenton R.G.; Cling M. Back R.J., Meller C.J., Fenton B.G.; Plochem. Biophys. Res. Commun. 202:549-555(1994).
                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                             ARGJ THETN
YD55 METJA
SYD PSEAE
SYD PSEPK
DBP9 YEAST
LEPA CHLTE
HELI HSVSA
                             SRA1 CAEEL
ALF TRYBB
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Genome Res. 10:758-775(2000).
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de Smet C., Brasseur F., van der Bruggen P., Lethe B., Lurquin C.,
Brasseur R., Chomez P., de Backer O., Cavenee W., Boon T.;
"Structure, chromosomal localization, and expression of 12 genes of
                                                                                                           MEDLINE=94311935; PubMed=8037761;
                                       the MAGE family.";
Immunogenetics 40:360-369(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U10687; AAA68871.1; -.
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PIR; 138661; 138661.
PDB; 114F; 25-JUL-01.
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                                                                                                                                                                                                                                                  Gene 160:287-290(1995).
                                                                                                                                                                                                                                     rejection antigens.
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                  SEQUENCE FROM N.A.
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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation for Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                      Schultz-Thater E., Junetic A., Dellabona P., Luscher U., Siegrist W., A Harder F., Heberer M., Zuber M., Spagnoli G.C.;

That agene product is a cytoplasmic protein.";

Int. J. Cancer 59:435-439(1994).

-!- FUNCTION: Not known, though may play a role in embryonal development and tumor transformation or aspects of tumor progression. Antigen recognized on a melanoma by autologous cytolytic T lymphocytes.

C. -!- SUBCELLULAR LOCATION: Cytoplasmic.

C. -!- SUBCELLULAR LOCATION: Antigen several types, carcinoma and breast carcinoma, but not in normal tissues except for testes. Never expressed in kidney tumors, leukemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Melanoma-associated antigen 4 (MAGE-4 antigen) (MAGE-X2) (MAGE-41)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95012457; PubMed=7927540;
de Plaen E., Arden K., Traversari C., Gaforio J.J., Szikora J.-P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/FIId=VAR_004283.

72 R -> Q (in dbSNP:2008144).
/FIId=VAR_011737.

163 D->A: ABOLISHES HIA-A1 BINDING.
169 Y->A: ABOLISHES HIA-A1 BINDING.
34342 MW, 544EEBIF9F4E9D33 CRC64;
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DOMAIN 102 301 MAGE.
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Pred. No. 4.2e-06;
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                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (Se or send an email to license@isb-sib.ch).
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              MEDLINE=95012905; PubMed=7927954;
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01-NOV-1995 (Rel. 32, Last seq
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SUBCELLULAR LOCATION
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Blood;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MUTAGEN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAG4 HUN
P43358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAG4_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Duodenum;

X Straubberg R.L., Feingold E.A., Gruce L.H., Derge J.G.,

Betausberg R.L., Feingold E.A., Gruce, L.H., Derge J.G.,

Ratausberg R.L., Feingold E.A., Gruce, L.H., Schamer G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

An Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Bronstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Raha S.S., Worley M., Sodergren E.J., Lu X., Gibbs R.A.,

Raha S., World W., Schergen E.J., Lu X., Gibbs R.A.,

Raha S., World W., Schermen J.W., Schwutz J., Myers R.M.,

Blakesley R.W., Touchman J.W., Schwutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

Reneration and initial analysis of more than 15,000 full-length

Proc. Natl. Acad. Sci. US.A. 99:16899-16903(2002).

PEVELOPHENT AND TUWOR TRANSFORMATION OR ASPECTS OF TUMOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002190; MAGE.
Pfam; PP01454; MAGE; 1.
PROSITE; PS50838; MAGE; 1.
Antigen; Multigene family; Polymorphism; Tumor antigen; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL TYPES, SUCH AS MELANOMA, HEAD AND NECK SQUAMOUS CELL CARCINOMA, LUNG CARCINOMA AND BREAST CARCINOMA, BUT NOT IN NORMAL TISSUES EXCEPT
                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDILIDE-953.69706; PubMed-7642112;
Imai Y., Shichijo S., Yamada A., Katayama T., Yano H., Itoh K.;
"Sequence analysis of the MAGE gene family encoding human tumor-
Ding M., Beck R.J., Keller C.J., Fenton R.G.; "Cloning and analysis of MAGE-1-related genes."; Biochem. Biophys. Res. Commun. 202:549-555(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: Contains 1 MAGE domain.
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NON TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Int. J. Syst. Bacteriol. 46:1004-1009(1996).
                                                                                                                  Gaps
                                                                                                                                                                                                                                                                    15-DEC-1998 (Rel. 37, Last sequence update)
DNA-bEC-1998 (Rel. 37, Last annotation update)
DNA-directed RNA polymerase beta' chain (EC 2.7.6) (Transcriptase beta' chain) (RNA polymerase beta' subunit) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                          Morse R., Collins M.D., O'Hanlon K., Wallbanks S., Richardson P.T., "Analysis of the beta' subunit of DNA-dependent RNA polymerase does not support the hypothesis inferred from 16S rRNA analysis that Cencoccus oeni (former!) Leuconostoc oenos) is a tachytelic (fast-evolving) bacterium."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - {RNA} [NU].
- 1- SUBDINIT: The enzyme consists of the sigma chain and the core enzyme which is composed of 2 alpha chains, 1 beta chain, and 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of DNA into RNA using the four ribonucleoside triphosphates as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: Belongs to the RNA polymerase beta' chain family.
                                                                                                                  ö
                                                                                      75.7%; Score 56; DB 1; Length 317; 73.3%; Pred. No. 0.0089; ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF04997; RNA_pol_Rpb1_1; 1.
Pfam; PF00623; RNA_pol_Rpb1_2; 1.
Pfam; PF006393; RNA_pol_Rpb1_3; 1.
Pfam; PF04999; RNA_pol_Rpb1_4; 1.
Pfam; PF04999; RNA_pol_Rpb1_5; 1.
SMART; SM00663; RPOLA, N; 1.
ZMART; SM00663; RPOLA, N; 1.
Transferase; DNA-directed RNA polymerase; Transcription.
                          T -> A.
/FTId=VAR_004284.
E -> Q (IN REF. 2).
3CFAC0E2B696257C CRC64;
                                                                                                                                                                                                                                                                                                                       Oenococcus oeni (Leuconostoc oenos).
Bacteria; Firmicutes; Lactobacillales; Oenococcus.
                                                                                                                                                                                                                                 PRT; 1004 AA
              POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000722; RNA pol A.
InterPro; IPR007080; RNA pol Rpbl 1.
InterPro; IPR007086; RNA pol Rpbl 3.
InterPro; IPR007083; RNA pol Rpbl 4.
InterPro; IPR007081; RNA pol Rpbl 5.
InterPro; IPR00592; RNA pol Rpbl 5.
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-NCDO 1674;
MEDLINE-97016803; PubMed-8863429;
                                                                                                                                                                                                                                                           Created)
                                                              317 AA; 34929 MW;
                                                                                                                                                        285 VKVLEHVVRVNARVR 299
                                                                                                                                         1 VKVLEYVIKVSARVR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X96384; CAA65248.1; -.
                                                                                                                Conservative
                                                                                                                                                                                                                                STANDARD;
 309
44
173
                                                    307
                                                                                                    Local Similarity
les 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              beta' chain.
              41
                                                  307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                substrates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; Q9KWU6;
                                                                                                                                                                                                                                                       15-DEC-1998 (15-DEC-1998 (15-DEC-1998 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ē
                                                                                                                                                                                                                   RPOC_OENOE
ID RPOC_OENOE
AC P95405;
                                                 CONFLICT
DOMAIN
DOMAIN
VARIANT
                                                                                        Query Match
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                                                                                                      Best Loc
Matches
                                                                                                                                                                                                         RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable tRNA (5-methylaninomethyl-2-thiouridylate)-methyltransferase
                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transferase, Methyltransferase, tRNA processing, Complete proteome
SEQUENCE 364 AA; 41666 MW; 2DCAC865A65BC071 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

STRAIN=MB4 / JCM 11007;

MEDLINE=21992816; PubMed=11997336;

MEDLINE=21992816; PubMed=11997336;

Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong W., Yang J.

Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling

Tan H., Chen R., Wang J., Yu J., Yang H.;

A complete sequence of T tengcongensis genome.";

Genome Res. 12:689-70(2002).

-!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + tRNA = S-aden

homocysteine + tRNA containing 5-methylaminomethyl-2-
                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                             Length 1004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thermoanaerobacter tengcongensis.
Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51.4%; Score 38; DB 1; Length 364;
1004 1004
1004 AA; 111965 MW; 73750DF47F3A2C36 CRC64;
                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLUIAR LOCATION: Cytoplasmic (By similarity). SIMILARITY: Belongs to the trmU family.
                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Clostridia; Thermoanae:
Thermoanaerobacteriaceae; Thermoanaerobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          493 AA
                                                                                                                                3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 21;
6; Mismatches
                                                                                                        40;
                                                                             Score 39;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF03054; tRNA Me trans; 1.
TIGRFAMS; TIGR00420; trmU; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE013086; AAM24468.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      396 IEKLEEEIKVTAKIRY 311
                                                                             52.7%;
63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VKVLEYVIKVSARVRF 16
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InterPro; IPR004506; TrmU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 43.8
Matches 7; Conservative
                                                                                                                                                                                                              ||||::|||:|
942 EYVLPISARLR 952
                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                   5 EYVIKVSARVR 15
                                                  Query Match
Best Local Similarity
7; Conserv?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=119072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thiouridylate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (EC 2.1.1.61).
TRMU1 OR TTE1243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001
16-OCT-2001
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                              TRU1 THETN
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067868;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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HAMAP; MF 00172; -; 1.

InterPro; IPR006276; Met syn B12ind.

InterPro; IPR006269; Methionine synth.

Pfam; PF01717; Methionine synt; 1.

Prodom; PD046829; Methionine synt; 2.

TIGRPAMS; TIGR01371; met syn B12ind; 1.

Transferase; Methyltransferase; Methionine biosynthesis; Zinc; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           formation (By similarity).
-!- CATALYTIC ACTIVITY: 5-methyltetrahydropteroyltri-L-glutamate + L-homocysteine = tetrahydropteroyltri-L-glutamate + L-homocysteine = tetrahydropteroyltri-L-glutamate + L-methionine.
-!- COFACTOR: Zinc; binds one ion per subunit (By similarity).
-!- PATHWAX: Terminal step in the de novo biosynthesis of methionine.
-!- SIMILARITY: Belongs to the vitamin-B12 independent methionine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Hypothetical protein Rv1461/WHT508/Mb1496 [Contains: Endonuclease PI-MtuHIIP (EC 3.1.-.-) (Mtu pps1 intein)].
RV1461 OR MISO8 OR MYV007.08 OR MB1496.
      (EC 2.1.1.14) (Methionine synthase, vitamin-B12 independent isozyme)
(Cobalamin-independent methionine synthase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 392:353-358(1998).
-!- FUNCTION: Catalyzes the transfer of a methyl group from 5-
methyltetrahydrofolate to homocysteine resulting in methionine
                                                                                                                                                                                                                                                                                                                              Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Garham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber Feldman R.A., Short J.M., Olson G.J., Swanson R.V., "The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 38; DB 1; Length 761;
Pred. No. 46;
4; Mismatches 2; Indels
                                                                                                                           Bācteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
NCBI_TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
C8F69759F86D5383 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773, 1765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             846 AA.
                                                                                                                                                                                                                                                                                               MEDLINE=98196666; PubMed=9537320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium tuberculosis, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE000752; AAC07565.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88631 MW;
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Best Local Similarity 57.1%;
Matches 8; Conservative
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645
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                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome.
                                                                                                    Aquifex aeolicus.
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729
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053152;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the buspean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1. CATALYTIC ACTIVITY: Release of an N-terminal amino acid, Xaa- | - Xbb-, in which Xaa is preferably Leu, but may be other amino acids including Pro although not Arg or Lys, and Xbb may be Pro. - COFACTOR: Binds 2 manganese ions per subunit (By similarity). - SUBCELLULAR LOCATION: Cycoplasmic (By similarity). - SIMILARITY: Belongs to peptidase family M17.
   Probable cytosol aminopeptidase (EC 3.4.11.1) (Leucine aminopeptidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R MENOPS; MI.UPW; -.

IR HAMAP; MF_00181; -; 1.

IR HAMAP; MF_00181; -; 1.

IR HAMAP; MF_00181; -; 1.

IR InterPro; IPR000813; Peptidase_MI7_N.

IR PR03789; Peptidase_MI7; I.

IR PR03789; Peptidase_MI7; I.

IR PR0371E; PR00481; LawNoPPTDASE.

IR MYCOLAGE; Aminopeptidase; Manganese; Complete proteome.

FT METAL 267 267 MANGANESE 18Y SIMILARITY).

FT METAL 280 280 MANGANESE 18Y SIMILARITY).

FT METAL 280 280 MANGANESE 18Y SIMILARITY).

FT METAL 339 339 MANGANESE 1 (BY SIMILARITY).

METAL 339 339 MANGANESE 1 (BY SIMILARITY).

"OFFICE OF MANGANESE 1 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
38-FEB-2003 (Rel. 41, Last annotation update)
5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase
                                                                                                                                                                                                                                                                                                                       Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Shead M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; Inthe complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- FUNCTION: Presumably involved in the processing and regular turnover of intracellular proteins. Catalyzes the removal of unsubstituted N-terminal amino acids from various peptides (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
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                                                        PEPA OR AC 2009.
Aquifex aeolicus.
Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                            MEDLINE=98196666; PubMed=9537320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE000772; AAC07829.1; -. PIR; H70479; H70479.
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             (Leucyl aminopeptidase)
R AQ_2099.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 392:353-358(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 LEYVIKVSARV 14
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493 AA;
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MEROPS; M17.UPW; -.
                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                          NCBI_TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similarity)
                                                                                                                                                                                                                                                                 STRAIN=VF5;
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067606;
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SEQUENCE
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BUNGOON WARANTANA WARANTAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

CALLES-M. Luberculosis; STRAIN-H37Rv;

MEDLINE=98295987; PubMed=9634230;

A Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Cole S.T., Brosch R., Parkhill J., Brown D., Chillingworth T., Cornor R., Badcock K., Basham D., Brown D., Chillingworth T., Cornor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., A. Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Seeger K., Skelton S., Squares S., Squares R., Sulgron J.E., Taylor K., Whitehead S., Barrell B.G.;

T. Deciphering the biology of Mycobacterium tuberculosis from the Complete genome sequence.";
                                                                                                                                                                                                                                                                          SPECIES=M.cuberculosis; STRAIN=CDC 1551 / Oshkosh;
MEDLINE=22206494; PubMed=12218036;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Kolonay J.F., Delson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J.A., Khouri H., Gill J., Mikula A.,
Bishal W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
"Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                    Harris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tubercutist; Rv1461;
InterPro; IPR003587; Hedgehog hint N.
InterPro; IPR003586; Hedgehog hintC.
InterPro; IPR007868; Hom end hint.
InterPro; IPR006142; INTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IIGRFAMs; TIGR01443; intein_Cterm; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR004042; Intein_endonuc.
InterPro; IPR006141; Intein_S.
InterPro; IPR000825; UPF0051.
                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteriol. 184:5479-5490(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, AL021184; CAA15991.1; --
EMBL, AE007020; AAK45772.1; --
EMBL, BX248339; CAD96163.1; --
PIR, H70871, H70871,
HSSP, P17255; 1VDE.
REBASE, 4211; PI-MtuHIIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF05203; Hom end hint; 1.
Pfam; PF01458; UPF0051; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                endonuclease family.
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SMART; SM00305; HintC; 1
SMART; SM00306; HintN; 1
                                                                                                                                                                                                                                                                                                                                                                                                                  laboratory strains."
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                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-1128732; PubMed=11234002;
A Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
A WEDLINE-1128732; PubMed=11234002;
A Webelar P.K., Hornore N., Garnier T., Churcher C., Harris D.,
A Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
A Rutter S., Seeger K., Gimon S., Simmonds M., Skelton J., Squares R.,
Barrell B.G.,
A Barrell B.G.,
I Mature 409:1007-1011(2001).
I Nature 409:1007-1011(2001).
I Dept. PPM: This protein undergoes a protein self splicing that involves a post-translational excision of the intervening region (intein) followed by peptide ligation (Potential).

- I SIMILARITY: Belongs to the UPPF0051 (ycf24) family.
                                                                                                                                                                                                                                                           Gaps
PROSITE; PS50818; INTEIN C_TER; 1.
PROSITE; PS50819; INTEIN_N_TER; 1.
PROSITE; PS50817; INTEIN_N_TER; 1.
Hypothetical protein; Protein splicing; Autocatalytic cleavage;
Hydrolase; Nuclease; Endonuclease; Intron homing; Complete proteome.
Thydrolase; Nuclease; Hypotherical PROTEIN RV1461, 1ST PART
                                                                                                                        (FOTENTIAL).
ENDONUCLEASE PI-MTUHIIP (POTENTIAL).
HYPOTHETICAL PROTEIN RV1461, 2ND PART
                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium leprae.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                     Score 38; DB 1; Length 846;
Pred. No. 51;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Smith D.R., Robison K.;
Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                               049689; 033141;
15-JUL-1998 (Rel. 36, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FBE-2003 (Rel. 41, Last sennotation update)
Hypothetical protein MLO593 (Contains: Mle pps1 intein)
MLO593 OR MLCL536.28C OR B1496_C2_189.
                                                                                                                                                                                      468CEEF979B02222 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                      869 AA.
                                                                                                                    (POTENTIAL)
                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                      846 AA; 94171 MW;
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EMBE, 729125; CABIGIT1.1; -.
EMBL, ALS89129; CAC30101.1; -.
PIR, 886983; A86983.
PIR, 572760; 572760.
                                                                                                                                                                                                                        51.4%;
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626 VVEIIVKPHARVRY 639
                                                                                                                                                                                                   Query Match
Best Local Similarity 50.00,
                                                                                                                                                                                                                                                                                          VLEYVIKVSARVRF 16
                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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846
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612
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                                                                                                                                                                                      SEQUENCE
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            RARARITITES
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NCBI_TaxID=1769;
                           TIGR; BB0115;
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Q9CCS6;
                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAINS-ATCC 35210 / B31;
STRAINS-ATCC 35210 / B31;
MEDLINE-98065943; PubMed=9403685;
Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
Dougherty B., Tomb J.F., Fleischmann R.D., Richardson D.,
Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
Utterback T., Watthey L., McDonald L., Arriach P., Bowman C.,
Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Smith H.O., Vencer J.C.,
"Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                HYPOTHETICAL PROTEIN ML0593, 1ST PART
                                                                                                                                                                                                                                                     2ND PART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity).
-!- SIMILARITY: Belongs to the S6P family of ribosomal proteins.
                                                                                                                                               PROSITE; PS50818; INTEIN C TER; 1.
PROSITE; PS50819; INTEIN ENDONUCLEASE; 1.
PROSITE; PS50817; INTEIN N TER; 1.
Hypothetical protein; Autocatalytic cleavage; Protein splicing;
                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 390:580-586(1997).
-!- FUNCTION: Binds together with S18 to 16S ribosomal RNA (By
                                                                                                                                                                                                                                                                                                              Score 38; DB 1; Length 869;
Pred. No. 52;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                      MLE PPS1 INTEIN (POTENTIAL). HYPOTHETICAL PROTEIN ML0593,
                                                                                                                                                                                                                                                             (POTENTIAL).
A -> R (IN REF. 1).
DB04CF70CB50765A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
30S ribosomal protein S6.
RPSF OR BB0115.
                                                                                                                                                                                                                             (POTENTIAL).
                    InterPro; INTEROGETAC; INTERN.
InterPro; IPROGETAC; INTERN.
InterPro; IPROGETA; Intein_endonuc.
InterPro; IPROGETA; Intein_S.
InterPro; IPROGETA; INTEIN_S.
Pfam; PFO1458; UPFO051; 1.
SWART; SWO0305; HINTC; 1.
                                                                                                                        TIGREAMs; TIGRO1443; intein_Cterm; 1.
TIGRFAMs; TIGR01445; intein_Nterm; 1.
InterPro; IPR003587; Hedgehog hint N.
InterPro; IPR003586; Hedgehog hint C.
                                                                                                                                                                                                                                                                                        95573 MW;
                                                                                                                                                                                                                                                                                                              51.4%;
                                                                                                                                                                                                                                                                                                                                                                            |:| ::| |||||
649 VVEIIVKPHARVRY 662
                                                                                                                                                                                                                                                                                                                                                               3 VLEYVIKVSARVRF 16
                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 50.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                       587
869
                                                                                                                                                                                                              201
                                                                                                                                                                                                                                                                         482 4
869 AA;
                                                                                                                                                                                                    Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  RS6_BORBU
O51142;
15-DEC-1998 (
15-DEC-1998 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            burgdorferi
                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                    CHAIN
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RS6_BORBU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor N. Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Rutherter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Barrell B.G.; Woodward J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Chorismate synthase (EC 4.2.3.5) (5-enolpyruvylshikimate-3-phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
-!- CARALVITIC ACTIVITY: 5-O-(1-carboxyvinyl)-3-phosphoshikimate
chorismate + phosphate.
-!- COFACTOR: Reduced flavin (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium leprae.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                             Score 37; DB 1; Length 139;
Pred. No. 12;
2; Mismatches 5; Indels
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-!- SIMILARITY: Belongs to the chorismate synthase family.
                                                                                           HAWAP, MF 00360; -; 1.

InterPro; IPR000529; Ribosomal_S6.
Pfam; PF01250; Ribosomal_S6; 1.

TIGRFAMS; TIGR00166; S6; 1.

PROSITE; PS01048; RIBOSOMAL_S6; FALSE NEG.
Ribosomal protein; rRNA-binding; Complete proteome.

SEQUENCE 139 AA; 16437 MM; D21244ACBC8E2312 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    407 AA
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InterPro; IPR00453; Chorismate_synth.
Pfam; PF01264; Chorismate_synt, 1.
Probom; PD002941; Chorismate_synt; 1.
TIGRFAMs; TIGR00033; aroC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21128732; PubMed=11234002;
                                                                                                                                                                                                                                                                                                                                                 50.0%; Scc...
53.3%; Pred
2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last seq
28-FEB-2003 (Rel. 41, Last ann
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EMBL; AE001123; AAC66491.1;
PIR; C70114; C70114.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 KVLEYVIKVSARVRF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : ||| || || ||
45 RALEYPIKKQARGRY 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             phospholyase).
AROC OR AROF OR ML0516.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; D86973; D86973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Leproma; ML0516; -.
                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seventh step.
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SYD PSESM
    Query Match
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                                                                                                                                                                                                                        (AspRS)
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                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-ATCC 25586,

MEDLINE-21886394; PubMed=11889109;

MEDLINE-21886394; PubMed=11889109;

MEDLINE-21886394; PubMed=11889109;

MEDLINE-21886394; PubMed=11889109;

MEDLINE-21886394; PubMed=11889109;

MEDLINE-21886394; PubMed=11889109;

Nagheran V., Anderson I., Ivanova N., Grechkin G., Los T., Lykidis A.,

Nasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A.,

A Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,

Ponstein M., Kyrpides N., Overbeek R.;

"Genome sequence and analysis of the oral bacterium Fusobacterium

"Genome sequence and analysis of the hypermodified nucleoside 5-

"Involved in the biosynthesis of the hypermodified nucleoside 5-

methylaminomethyl-2-thiouridine, which is found in the wobble

position of some tRNAs (By similarity).

"In SIMILARITY: Belongs to the era/trmE family of GTP-binding

proteins. TrmE subfamily.
                                                                                                        Gaps
                                                                                                        ö
PROSITE; PS00787; CHORISMATE_SYNTHASE_1; 1.
PROSITE; PS00788; CHORISMATE_SYNTHASE_2; 1.
PROSITE; PS00789; CHORISMATE_SYNTHASE_3; 1.
Lyase; Aromatic amino acid biosynthasis; Complete proteome.
SEQUENCE 407 Aa; 42473 MW; 1F677D07ADB556AF CRC64;
                                                                             Length 407;
                                                                                                                                                                                                                                                                                                                           Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
                                                                                                       5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8BE4CE1F983B76B3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 37:

    Created)
    Last sequence update)
    Last annotation update)

                                                                                                                                                                                                                                                                                                             Fusobacterium nucleatum (subsp. nucleatum).
                                                                                                    4; Mismatches
                                                                          50.0%; Score 37; 43.8%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAMAP; MF_00379; -; 1.
InterPro; IPR005289; GTP-bindding_dom.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGRFAMS; TIGRO0650; MG442; 1.
TIGRFAMS; TIGRO0231; small GTP; 1.
TIGRFAMS; TIGRO0450; thdF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR006073; GTP1_OBG.
InterPro; IPR0052917; MMR_HSR1.
InterPro; IPR005225; Small_GTP.
InterPro; IPR004520; ThdF.
                                                                                                                                                                                                                                            28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last seq 28-FEB-2003 (Rel. 41, Last ann tRNA modification GTPase trmE. TRME OR FN0006.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE010516; AAL94219.1; -.
                                                                                                                                             |:|| :|| :| |:
161 VEVLSHVISIGASARY 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50630 MW;
                                                                                                                               1 VKVLEYVIKVSARVRF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF01926; MMR HSR1; 1.
PRINTS; PR00326; GTP10BG.
                                                                                        Best Local Similarity 43.8 Matches 7; Conservative
                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             333 3
455 AA;
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=ATCC 25586;
                                                                                                                                                                                                                                                                                                                                      Fusobacterium.
NCBI_TaxID=76856;
                                                                                                                                                                                                                      TRME FUSNN
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NP_BIND
SEQUENCE
                                                                            Query Match
                                                                                                                                                                                            RESULT 11
TRME_FUSNN
  8 K B B B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diphosphate + L-aspartyl-tRNA(Āsp).
--- SUBUMT: Homodimer (By similarity).
--- SUBCELLULAR LOCATION: Cytoplasmic.
--- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50862; AA TRNA LIGASE II; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Buell C.R., Joacfar V., Lindeberg M., Selengut J., Paulsen I.T., Gwinn M.L., Dodson R.J., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R., Daugharty S., Brinkac L., Beanan M.J., Haft D.H., Nelson W.C., Davidsen T., Zafar N., Zhou L., Liu J., Yuan Q., Khouri H., Fedorova N., Tran B., Russell D., Berry K., Utterback T., Van Aken S.B., Feldblyum T.V., D'Ascenzo M., Deng W.-L., Ramos A.R., Alfano J.R., Cartinhour S., Chatterfee A.K., Delaney T.P., Harto G., Martin G.B., Schneider D.J., Tang X., Bender C.L., White O., Fraser C.M., Collmer A., The complete genome sequence of the Arabidopsis and tomato pathogen Proc. Natl. Acad. Sci. US.A. 100:10181-10186(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                               15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Aspartyl-tRNA synthetase (EC 6.1.1.12) (Aspartate--tRNA ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pseudomonas syringae (pv. tomato).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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   Length 455;
                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4A841555305FBF36 CRC64;
Score 37; DB 1;
Pred. No. 41;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                      591 AA
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InterPro; IPR004115; GAD dom.
InterPro; IPR004364; TRNA-synt_2.
InterPro; IPR004365; TRNA-synt_asp.
InterPro; IPR004365; TRNA-anti.
Pfam; PF02938; GAD; 1.
Pfam; PF00152; TRNA-synt_2; 1.
Pfam; PF00136; TRNA-anti; 1.
Pfam; PF0136; TRNA-synt_2; 1.
                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22834015; PubMed=12928499;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66351 MW;
                             61.5%;
                                                                                                                                                               |||| |:| ||:
| KVLEVVLKNGARI 108
                                                                                                                           2 KVLEYVIKVSARV 14
                             Best Local Similarity 61.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGR; PSPT03981; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASPS OR PSPT03981.
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SEQUENCE 591 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=323;
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| :||||| :
241 VSPYDYVLQVSGRVEY 256
                                                                                                                                                                                                                                                                                                                                                                                     1 VKVLEYVIKVSARVRF 16
                                                                                                                                                                                                                                                                                                                                     50.08;
                                                                                                                                                                                                                                                                                                                                                43.8%;
                                                                                                                                                                                                                                                                                                                                                              7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=X2180-1A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YEAST
                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                       01-NOV-1995 (Rel. 32, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit, beta
1soform (EC 2.7.1.153) (PI3-kinase pll0 subunit beta) (PtdIns-3-kinase
pll0) (PI3K) (PI3Kbeta).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 4
                                                                                                                                                                                                                                                                                                                                                       KOSSILA M., Sinkovic M., Karkkainen P., Laukkanen M.O., Miettinen R., Rissanen J., Kekalainen P., Kuusisto J., Yla-Herttuala S., Laakso M.; Rissanen J., Kekalainen P., Kuusisto J., Yla-Herttuala S., Laakso M.; Gene encoding the catalytic subunit pli0beta of human phosphatidylinositol 3-kinase: cloning, genomic structure and screening for variants in patients with type 2 diabetes.", Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PHOSPHORYLATES PTDINS, PTDINS4P AND PTDINS(4,5)P2 PRERERENCE FOR PTDINS(4,5)P2.
--- FUNCTION: PACTIVITY: ATP + 1-phosphatidyl-1D-myo-inositol 4,5-bisphosphate = ADP + 1-phosphatidyl-1D-myo-inositol 3,4,5-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- PATHWAY: Signaling pathways regulating cell growth.
-!- SUBUNIT: HETERODIMER OF A P110 (CATALYTIC) AND A P85 (REGULATORY)
                                                                                                                                                                                                                                                                       MEDINE-94067128; PubMed-8246984;
Hu P., Mondino A., Skolnik E.Y., Schlessinger J.,
"Cloning of a novel, ubiquitously expressed human
phosphatidylinositol 3-kinase and identification of its binding site
                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO:0016303; F:phosphatidylinositol 3-kinase activity; TAS. GO:0000187; P:activation of MAPK; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- TISSUE SPECIFICITY: Expressed ubiquitously.
                                                                                     1070 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (Se
or send an email to license@isb-sib.ch).
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AJ297550; CAC21449.1; JOINED.
AJ297551; CAC21449.1; JOINED.
                                                                                                             (Rel. 32, Created)
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AJ297553; CAC21449:1; U
AJ297555; CAC21449:1; U
AJ297555; CAC21449:1; U
AJ297556; CAC21449:1; U
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CAC21449.1;
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CAC21449.1;
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                                                                                    STANDARD;
EYVIKVSARVR 15
                        EYVVKVVGKVR 77
                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 trisphosphate.
                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                P11B HUMAN P42338;
                                                                                                           01-NOV-1995
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PIR; A54
Genew; H
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PIK3CB.
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EMBL;
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EMBL;
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GO:0006935; P:chemotaxis; TAS.
GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
GO:0000074; P:regulation of cell cycle; TAS.
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01-NOV-1990 (Rel. 16, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Fatty acid synthase subunt alpha (EC 2.3.1.86) [Includes: Acyl carrier; 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100)
(Beta-ketoacyl reductase); 3-oxoacyl-[acyl-carrier protein] synthase (EC 2.3.1.41) (Beta-ketoacyl synthase)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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MEDLINE=97313271; PubMed=9169875;
Bussey H., Storms R.K., Ahmed A., Albermann K., Allen E., Ansorge Araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V., Botstein D., Bowman S., Bruckner M., Carpenter J., Cherry J.M., Chung E., Churcher C.M., Coster F., Davis K., Davis R.W., Dietrich F.S., Delius H., DiPaolo T., Dubois E., Duesterhoeft A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
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Pred. No. 99;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1887 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
                                                                                             InterPro; IPR008938; ARM.
InterPro; IPR008938; ARM.
InterPro; IPR008938; ARM.
InterPro; IPR008973; C2 Calb.
InterPro; IPR003420; P13 P14 kinase.
InterPro; IPR00313; P13K_C2.
InterPro; IPR00313; P13K_P85B.
InterPro; IPR00313; P13K_rss_bind.
InterPro; IPR001363; P13K_rss_bind.
InterPro; IPR001363; P13K_rss_bind.
InterPro; IPR001363; P13K_rss_i.
Pfam; PF00454; P13K_Rb5; 1.
Pfam; PF006192; P13K_rbd; 1.
SMART; SM00142; P13K_rbd; 1.
SMART; SM00144; P13K_rbd; 1.
SMART; SM00145; P13Ka; bd; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00915; PI3 4 KINASE 1; 1.
PROSITE; PS00916; PI3 4 KINASE 2; 1.
PROSITE; PS00290; PI3 4 KINASE 3; 1.
Transferase; Kinase; Multigene family.
DOMAIN 800 1050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   altered fatty acid synthase gene.";

Mol. Gen. Genet. 244:90-96(1994).

I altered fatty acid synthase gene.";

Mol. Gen. Genet. 244:90-96(1994).

-!- FUNCTION: Fatty acids from acetyl-CoA, malonyl-CoA and NADPH.

C long-chain fatty acids from acetyl-CoA, malonyl-CoA and NADPH.

The alpha subunit contains domains for: acyl carrier protein.

3-oxoacyl-lacyl-carrier protein] reductase, and 3-oxoacyl-(acyl-carrier-protein] synthase. This subunit coordinates the binding of the six beta subunits to the enzyme complex.

-!- CATALYTIC ACTIVITY: Acetyl-CoA + N CO(2) + 2N NADPH = a long-chain acyl-CoA + N CO(2) + 2N NADPH = a carrier protein] = 3-oxoacyl-[acyl-carrier protein] + malonyl-(acyl-carrier protein] + malonyl-(acyl-carrier protein] + 3-oxoacyl-[acyl-carrier protein] + CO(2) + CATALYTIC ACTIVITY: Acyl-carrier protein] + CO(2) + CATALYTIC ACTIVITY: Acyl-carrier protein] + CO(2) + CATALYTIC ACTIVITY: (3)-3-dydroxyacyl-[acyl-carrier protein] + CO(2) + CATALYTIC ACTIVITY: (3)-3-dydroxyacyl-[acyl-carrier protein] + NADPH.

-!- CATALYTIC ACTIVITY: (3)-3-dydroxyacyl-[acyl-carrier protein] + NADPH.

-!- CATALYTIC ACTIVITY: (3)-3-dydroxyacyl-[acyl-carrier protein] + CO(2) + CATALYTIC ACTIVITY: (3)-3-dydroxyacyl-[acyl-carrier protein] + NADPH.

-!- CATALYTIC ACTIVITY: (3)-3-dydroxyacyl-[acyl-carrier protein] + NADPH.

-!- CATALYTIC ACTIVITY: (3)-3-dydroxyacyl-[acyl-carrier protein] + NADPH.
Duncan M., Floeth M., Fortin N., Friesen J.D., Fritz C., Goffeau A., Hall J., Hebling U., Heumann K., Hilbert H., Hillier L.W., Kalman S., Kalman R., Johnston M., Kalman S., Kaleine K., Komp C., Kurdi O., Lashkari D., Lew H., Lin A., Lin D., Louis E.J., Marathe R., Messenguy F., Mewes H.-W., Mittipati S., Moestl D., Mueller-Auer S., Namath A., Nentwich U., Oefner P., Pearson D., Petel F.X., Pohl T.M., Purnelle D., Schafer M., Scharfe M., Scharfe M., Scharfe M., Urrestarazu L.A., Ushinsky S., Vierendeels F., Vissers S., Voss H., Walsh S.V., Wambutt R., Wang Y., Wedler E., Wedler H., Winnett E., Zhong W.W., Zollner A., Vo D.H., Hani J.; "The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI."; Nature 387:103-105(1997).
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BETA-KETOACYL REDUCTASE.
BETA-KETOACYL SYNTHASE.
PHOSPHOPANTETHEINE (BY SIMILARITY).
BETA-KETOACYL SYNTHASE (BY SIMILARITY).
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SIMILARITY: TO THE FATTY ACID SYNTHETASE, SUBUNIT ALPHA FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inokoshi J., Tomoda H., Hashimoto H., Watanabe A., Takeshima H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cerulenin-resistant mutants of Saccharomyces cerevisiae with an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         00606; B KETOACYL SYNTHASE; 1.
biosynthēsis; Multifunctional enzyme; Oxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00012; PHOSPHOPANTETHEINE; 1.
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EMBL; X76890; CAA44218.1; --
EMBL; X76890; CAA44218.1; --
EMBL; Z73586; CAA97947.1; --
EMBL; Z73587; CAA97947.1; --
EMBL; Z73587; CAA97948.1; --
EMBL; Z73587; CA
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MEDLINE=94316198; PubMed=8041367;
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MUTAGENESIS OF GLY-1250.
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Fransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Omura S.;
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ACT_SITE
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1QPRANIQLDFPELKPYKQVKQIAPAELEGLLDLERVI -->
CLNCVKSWLKLLKLERQFPSKLLWSIRLSMAIALMLKKS
KFNQELTFNWTSQNRNHTNRLNKLLPLSLRVCWIWKELF
                                             AKLRKELVETSEVRKAVSIETALEHKVVNGNSADAAYAQVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=94127588; PubMed=8051117;
Christiano A.W., Greenspan D.S., Uitto J.;
"Cloning of human type VII collagen. Complete primary sequence of the alpha 1(VII) chain and identification of intragenic polymorphisms.";
J. Biol. Chem. 269:20256-20262(1994).
                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=93107742; PubMed=1466284; Gammon W.R., Abernethy M.L., Padilla K.M., Prisayanh P.S., Cook M.E., Wright J., Briggaman R.A., Hunt S.W. III; "Noncollagenous (NCI) domain of collagen VII resembles multidomain extracellular matrix."; J. Invest. Dermatol. 99:691-696(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The large non-collagenous domain (NC-1) of type VII collagen is amino-terminal and chimeric. Homology to cartilage matrix protein, the type III domains of fibronectin and the A domains of von Willebrand factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 815-1439 FROM N.A.
MEDLINE-91334380; PubMed=1871109;
MEDLINE-91334380; PubMed=1871109;
Barente M.G., Chung L.C., Kyrnaenen J., Woodley D.T., Wynn K.W.,
Bauer E.A., Mattei M.-G., Chu M.-L., Uitto J.;
"Human type VII collagen: cDNA cloning and chromosomal mapping of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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MEDILES-93384371, PubMed=1307247;
Christiano A.M., Rosenbaum L.M., Chung-Honet L.C., Parente M.G.,
Woodley D.T., Pan T.C., Zhang R.Z., Chu M.-L., Burgeson R.E.,
                                                                                                                                                                                                                                                                                                                                                                                                      002388; Q14054; Q16507;
01-UNN-1994 (Rel. 29, Created)
01-FBB-1996 (Rel. 33, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Collagen alpha 1(VII) chain precursor (Long-chain collagen) (LC
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0
                                                                                                                                                                                                        Score 37; DB 1; Length 1887; Pred. No. 1.8e+02;
                                                                                                                         RWEMEA -> KMGNGS (IN REF. 1).
A -> S (IN REF. 1).
N -> T (IN REF. 1).
                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                          MW; 08B872734CF3AEEA CRC64;
G->S: CERULENIN-RESISTANCE.
                G -> GTTGTGG (IN REF. 1).
T -> I (IN REF. 1).
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                                                                                                             (IN REF. 1).
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Matches 8; Conservative
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"Structural organization of the human type VII collagen gene (COL7A1), composed of more exons than any previously characterized gene."; Genomics 21:169-179(1994),
               MEDLINE-92231902; PubMed=1567409;
Tanaka T., Takahashi K., Furukawa F., Imamura S.;
"Molecular cloming and blaracterization of type VII collagen cDNA.";
Biochem. Biophys. Res. Commun. 183:958-963(1992).
                                                                                                                                                                The carboxyl-terminal half of type VII collagen, including the non-
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MEDLINE-96081220; PubMed=8541842;
Christiano 6Al., Lee J.Y.-Y., Chen W.J., Laforgia S., Uitto J.;
"Pretibial epidermolysis bullosa: genetic linkage to COL7A1 and identification of a glycine-co-cysteine substitution in the triple-helical domain of type VII collagen.";
Hum. Mol. Genet. 4:1579-1583 (1995).
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Christiano A.M., Morricone A., Paradisi M., Angelo C., Mazzanti C.,
Cavalieri R., Uitto J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "A glycine-to-arginine substitution in the triple-helical domain of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98041666; PubMed=9375848; Jacryikallio A., Pulkkinen L., Uitto J.; Molecular basis of dystrophic epidermolysis bullosa: mutations in the type VII collagen gene (COL7A1)."; Hum. Mutat. 10:338-347(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT DEB LXS-2798.

WINDLINES-923291877; PubMed-8513326;
Christiano A.M., Greenspan D.S., Hoffman G.G., Zhang X., Tamai Y.,
Lin A.N., Dietz H.C., Hovnanian A., Uitto J.;
An Ansensem mutation in type VII collagen in two affected siblings
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                                                                                                                                                                                      collagenous NC-2 domain and intron/exon organization of the corresponding region of the COL7A1 gene."; Hum. Mol. Genet. 2:273-278(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mimicking peeling skin syndrome."; Arch. Dermatol. 125:633-638(1989)
                                                                                                                                 MEDLINE-93271985; PubMed-8499916;
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                                                                                                                                                                                                                                                                                                                                           J., Greenspan D.S.;
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MEDLINE=96220218; PubMed=8644729;

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"Some, but not all, glycine substitution mutations in COL/Al result in
intracellular accumulation of collagen VII, loss of anchoring
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MEDLINE=96183562; PubMed=8618018;
Christiano A.M., McGrath J.A., Uitto J.;
Influence of the second COL7A1 mutation in determining the phenotypic severity of recessive dystrophic epidermolysis bullosa.";
J. Invest. Dermatol. 106:766-770(1996).
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MEDINE=97358588; PubMed=9215684;
Winberg J.-O., Hammani-Hausali N., Nilssen O., Anton-Lamprecht I.,
Naylor S.L., Kerbacher K., Zimmermann M., Krajci P.,
Gedde-Dahl T. Jr., Bruckner-Tuderman L.;
Modulation of disease severity.
                                                                                                                                                                       Uitto J.;
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collagen result in a spectrum of dystrophic epidermolysis bullosa
phenotypes and patterns of inheritance.";
Am. J. Hum. Genet. 58:671-681(1996).
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Wordanian A., Rochat A., Bodemer C., Petit E., Rivers C.A., Prost
Fraitag S., Christiano A.M., Uitto J., Lathrop M., Barrandon Y.,
de Prost Y.;
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MEDLINE=88410969; PubMed=9740253;
KON A., Pulkkinen L., Ishida-Yamamoto A., Hashimoto I., Uitto J.;
"Novel CoL7A1 mutations in dystrophic forms of epidermolysis bullosa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96310789; PubMed=8757758; Dunnill M.G.S., McGrath J.A., Richards A.J., Christiano A.M., Uitto J., Pope F.M., Eady R.A.J.; "Clinicopathological correlations of compound heterozygous COL7A1 mutations in recessive dystrophic epidermolysis bullosa."; J. Invest. Dermatol. 107:171-177(1996).
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Hammami-Hauasli N., Schumann H., Raghunath M., Kilgus O., Luethi
Luger T., Bruckner-Tuderman L.;
                                                                                                                                                                   Shimizu H., McGrath J.A., Christiano A.M., Nishikawa T., Uitto J
"Molecular basis of recessive dystrophic epidermolysis bullosa:
genotype/phenotype correlation in a case of moderate clinical
severity.";
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J. Biol. Chem. 273:19228-19234(1998)
[22]
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                                                                                                                                                  MEDLINE=96154068; PubMed=8592061;
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J. Invest. Dermatol. 111:534-537(1998).
[23] VARIANT DEB ARG-1347.
WARIANTE-99019477; PubMed-9804332;
Terracina M., Posteraro P., Schubert M., Sonego G., Atzori F.,
                                                                                                                           Query Match 50.0%; Score 37; DB 1; Length 2944; Best Local Similarity 63.6%; Pred. No. 2.8e+02; Matches 7; Conservative 2; Mismatches 2; Indels
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Q9htw6 pseudomonas Q9htw6 pseudomonas O67840 aquifex aeo Q98zml bacteroides Q8xzn5 clostridium Q899f5 clostridium Q899f7 clostridium Q899f7 clostridium Q899f7 clostridium Q809y0 zygosacchar Q96w49 arabidopsis Q8xx15 clostridium Q9b128 cystosporog Q7xw39 oryza sativ Q9b128 cystosporog Q7xw39 cryza sativ Q9b128 cystosporog Q7xw39 cryza sativ Q9b128 cystosporog Q7xx16 sulfolobus Q98ym9 arabidopsis Q8yy80 homo sapien Q8pg93 xanthomonas Q8x16 clostridium Q9bx55 arabidopsis Q8x46 ctreptomyce Q97hm2 clostridium Q9ax55 arabidopsis Q9xx6 drosophia
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Hepatoma;
Sui Y., Ye J., Wu W.;
Sui Y., Ye J., Wu W.;
"Cloning of a new gene of MAGE family in human hepatocellular actionma.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF443295; AAL37897.1;
InterPro; IPR002199; MAGE.
InterPro; IPR002199; MAGE.
PrositE; PS50838; MAGE; 1.
SEQUENCE 316 AA, 35409 MW; A463A9A740A089DF CRC64;
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O67840
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Q8XN55
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O58509
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Q14798 homo sapien
Q9bur9 homo sapien
Q8c20 pyrobaculum
Q8c20 pyrobaculum
Q8c20 thermotoga
Q9c21 thermotoga
Q9cyg5 trypanosoma
Q9azi5 bacteriopha
Q9cyg5 oryza sativ
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Q9cyf2 pichia angu
Q7zrn4 chimpanzee
Q43391 arabidopsis
Q9c1f2 pichia angu
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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STRAIN=TLS / ATCC 49652 / DSM 12025;

MEDLINE=22103665; PubMed=12093901;

A Bisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,

A Dodson R.J., Deboy R., Gwinn M.L., Nelson W.C., Haft D.H.,

Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F.,

Holt I., Umayam L.A., Mason T., Brenner M., Shea T.P., Parksey D.,

A Holt I., Umayam L.A., T., Hansen C.L., Craven M.B., Radune D.,

Naerman W.C., Feldblyum T.V., Hansen C.L., Fraser C.M., Ketchum K.A.,

Vamathevan J., Khouri H., White O., Gruber T.M., Ketchum K.A.,

Vamathevan J., Tettellin H., Bryant D.A., Fraser C.M.,

The complete genome sequence of Chlorobium tepidum TLS, a

photosynthetic, anaerobic, green-sulfur bacterium...,

R FMBL; ABG12841; AAM71941.1;

R TIGR; CT0704;
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Miller J.H.;
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EMBL, AE009771; AAL62840.1; -.
GO; GO:0008969; F:phosphohistidine phosphatase activity; IEA.

InterPro; IPR00449; SixA.

TIGRPAMS; TIGR00249; sixA; 1.
                                                                                                                                                                                                                                                                                                                   Chlorobium tepidum.
Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
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GO; GO:0008270; F:inc ion binding; IEA.
GO; GO:000508; P:proteolysis and peptidolysis; IEA.
GO: PRO02725; DUFAS.
InterPro; IPR002725; Pept_M_Zn_BS.
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Last annotation update)
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01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       152 AA
                                                        248 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
                                                                                                                                 Created)
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STRAIN=IM2 / ATCC 51768 / DSM 7523;
MEDLINE=21664397; PubMed=11792869;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01863; DUF45; 1. - - PROSITE; PS00142; ZINC_PROTEASE; 1.
                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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Thermoproteaceae; Pyrobaculum,
NCBI_TAXID=13773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        O1-JUN-2003 (TrEMBLrel. 24, L. Hypothetical protein PAE0518.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protease; Complete proteome.
SEQUENCE 248 AA; 28214 MW
                                                                                                                                                                 (TrEMBLrel. 22, (TrEMBLrel. 25,
                                                                                                                         01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :|| :||| | |:
13 IEYTVKVSQRARY 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 LEYVIKVSARVRF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                PRELIMINARY;
                                                                                                                                                                                                                                                  protease, putative.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                NCBL_TaxID=1097;
                                                                                                                                                                                                          01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                    Chlorobium.
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                                                                                        Q8KEI5;
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                                                Q8KEI5
                                                                                                                                                                                                                                                                                          CT0704
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Q8ZZ01
            Q8KEI5
                                                        DDT TAPE TO THE PROPERTY OF TH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Skin antigen, family A, 8 (Melanoma antigen, family A, 8).
Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=95369706; PubMed=7642112;
Imai Y., Shichijo S., Yamada A., Katayama T., Yano H., Itoh K.;
Imai Y., Shichijo S., Yamada A., Katayama T., Yano H., Itoh K.;
"Sequence analysis of the MAGE gene family encoding human tumor-
rejection antigens.";
Gene 160:287-290(1995).
InterPro; IPR002190; MAGE.
InterPro; IPR002190; MAGE.
Pfam; PF0145; MAGE; I.
SEQUENCE 317 AA, 35044 MW; 9B9477253FB307C4 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 75.7%; Score 56; DB 4; Length 317; Best Local Similarity 73.3%; Pred. No. 0.068; Matches 11; Conservative 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 75.7%; Score 56; DB 4; Length 318; Best Local Similarity 73.3%; Pred. No. 0.068; Matches 11; Conservative 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
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        01, Last sequence update) 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    318 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |||||:|::|:||||
285 VKVLEHVVRVNARVR 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              287 VKVLEHVVRVNARVR 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 VKVLEYVIKVSARVR 15
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01-NOV-1996 (TrEMBLrel. 01-MAR-2003 (TrEMBLrel. MAGE-4 protein. MELANOMA ANTIGEN-4.
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PROSITE; PS50838; MAGE; SEQUENCE 318 AA; 352
                                                                                                                                                                 Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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TISSUE=Skin;
                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
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54.1%;
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69 EVLEYAVLVSARL 81
                                                                                                                                                                                                                                                                     Local Similarity 62.5
les 10; Conservative
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nes 8; Conservative
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Bacteriophage bIL310.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trypanosoma brucei.
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01-OCT-2003
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01-JUN-2001
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Matches
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Q9AZIS
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                                                                                                                                                                                                                                                                                                                                        Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., Read T.D., Bisen J.A., Seshadir R., Ward N., Methe B., Clayton R.A., Meyer T., Taapin A., Scott J., Beanan M., Brinker L., Daugherty S., DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Vamathevan R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Vamathevan J., Weldman J., Impraim M., Lee K., Berry K., Lee C., Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.; Shewanella oneidensis."
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                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thermotogae; Thermotogales; Thermotogaceae; Thermotoga
                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
Alteromonadaceae; Shewanella.
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STRAIN=MSB8 / DSM 3109;
MEDLINE=99287316; PubMed=10360571;
Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55.4%; Score 41; DB 16; Length 1390; 60.0%; Pred. No. 1.5e+02;
                              Length 152;
                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l protein; Complete proteome.
1390 AA; 152805 MW; 390BB26E255A60A8 CRC64;
           774D93701DF46720 CRC64;
                                                                                                                                                                                    01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein TM1741.
                               55.4%; Score 41; DB 17; 50.0%; Pred. No. 19;
                                                                                                                                                              PRT; 1390 AA.
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                                                        3; Mismatches
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Hypothetical protein; Complete proteome.
SEQUENCE 152 AA; 17097 MW; 774D93701
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nat. Biotechnol. 20:1118-1123(2002).
                                                                                                                                                                                                                                                                                                                               MEDLINE=22297686; PubMed=12368813;
                                                                                                                                                                                                                   Conserved hypothetical protein. SO4093.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE015840; AAN57067.1; -.
TIGR; SO4093; -.
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1244 KVLEPVIEVISEIRF 1258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16
                                                                              2 KVLEYVIKVSARVR 15
                                                                                            |: ||: ||:
33 KIAEYLAKIGVRVR 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR007844; AsmA.
Pfam; PF05170; AsmA; 1.
Hypothetical protein; Comp
                                            Best Local Similarity 50.0 Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 60.0°
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 KVLEYVIKVSARVRF
                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                              Shewanella oneidensis.
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                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                NCBI_TaxID=70863;
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                                  Query Match
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Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A., McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M., Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D., Heidelberg J., Sutton G.G., Pleischmann R.D., Eisen J.A., White O., Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.; Fraser C.M.; Fraser C.M.; Mute O., Nenter J.S., Essen J.A., White O., Neure 399.323-329(1999).

BMBL, AEO01812, AAD36806.1; -. PIGR, TM1741; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

Li Z., Wang C.C.;

Submitted (Aug. 2001) to the EMBL/GenBank/DDBJ databases.

Submitted (Aug. 2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF404120; AAL72635.1; -.

GO; GO:0005838; C:proteasome regulatory particle (sensu Eukarya); IEA.

GO; GO:0005698; P:proteolysis and peptidolysis; IEA.

InterPro; IPR006746; Ninl_C.

Pfam; PF04653; Ninl_C; 1.

SEQUENCE 274 AA; 31298 MW; 3FF0F1963953F83D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukāryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR004441; rRNA_methyl_3.
InterPro; IPR001537; SpoU methylase.
Pfam; PF00588; SpoU methylase; 1.
ProDom; PD001243; SpoU methylase; 1.
ProDom; PT0RPAMs; TCR0186; rRNA methylase; 1.
Hypothetical protein; Complete protecome.
BEQUENCE 242 AA; 27096 MW; 0369F95E1921D14 CRC64;
                                                                                                                                                                                                                                                                                                                                                        GO; GO:0003723; F:RNA binding; IEA.
GO; GO:0008173; F:RNA methyltransferase activity; IEA
GO; GO:0009451; P:RNA modification; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2002 (TrEMBLrel. 20, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Proteasome regulatory non-ATP-ase subunit 12.
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(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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Pred. No. 51;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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us-09-336-091-3.rspt

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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                            8; Conservative
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                                                                                                                                                                                                                                                                                                                     ANK repeat; Repeat.
SEQUENCE 568 AA;
                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                             SEQUENCE FROM N.A.
                                                                                        NCBI_TaxID=39947;
                                P0592G05.12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1999
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01-JUN-2003
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Q9X156
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"The complete genome sequence of the lactic acid bacterium Lactococcus lactis spp. lactis IL1403.";
Genome Res. 11:731-755(2001).
EMBL; AE006242; AAK04127.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                        Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
NCBI_TaxID=1360;
                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                         MEDLINE=21113149; PubMed=11160885;
Chopin A., Bolotin A., Sorokin A., Ehrlich S.D., Chopin M.-C.;
"Analysis of six prophages in Lactococcus lactis IL1403: different
genetic structure of temperate and virulent phage populations.";
Nucleic Acids Res. 29:644-651(2001).
dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                       Chopin A., Bolotin A., Sorokin A., Ehrlich S.D., Chopin M.-C.; Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF323671, AAK08428-1; -.
INTERPYC; IPR004568; POX D5.
InterPYC; IPR005500; Primase_C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 16; Length 542; 97;
                                                                                                                                                                                                                            Score 40; DB 9; Length 542; Pred. No. 97;
                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                  InterPro; IPRU000000, 1.
Pfam; PF03288; POx D5; 1.
TIGRO1613; primase_Cterm; 1.
TIGRO1613; primase_Cterm; 1.
TGRO1613; primase_Cterm; 1.
TGRO1613; primase_Cterm; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  542 AA; 62322 MW; 64CD85DE975CC5E4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Prophage ps1 protein 05, DNA primase.
PS105 OR LL0029.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3,
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                                                                                                                                                                                                                                                  4; Mismatches
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                                                                                                                                                                                                                            54.1%; Score 40; 50.0%; Pred. No.
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InterPro; IPR006500; Primase_C.
Pfam; PF03288; Pox D5; 1.
TIGRFAM8; TIGR01613; primase_Cterm; 1.
                                                                                                                                                                                                                                                                                                                                                     PRT;
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QBRYGS;
01-JUN-2002 (TrEMBLrel. 21, Created)
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                                                                                                                                                                                                                           Query Match
Best Local Similarity 50.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 50.0 tes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
          NCBI_TaxID=151538;
                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                            SEQUENCE FROM N.A.
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Matches
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QBRYGS
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Q9CJG6
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'Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, PAC
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Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Pleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
"Evidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                              Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga
NCBI_TaxID=2336;
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0
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Pred. No. 1e+02;
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                                                                                                                                                                                                                                                                                                                                                                         clone:P0552G05.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AP004672; BAB90826.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           568 AA; 64128 MW; 7E962344765200B3 CRC64;
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(TrEMBLrel. 12, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Mismatches
01-OCT-2003 (TrEMBLrel. 25, Last annotati
Anther ethylene-upregulated protein-like.
                                                                                                                                                                                                                                                                                       STRAIN=cv. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50088; ANK REPEAT; 1.
PROSITE; PS50297; ANK REP REGION; 1.
PROSITE; PS50096; IQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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MEDLINE=99287316; PubMed=10360571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gramene; Q8RYGS; ...
InterPro; IPR002110; ANK.
InterPro; IPR007110; Ig-like.
InterPro; IPR000048; IQ_region.
Pfam; PF00612; IQ, 3.
SMART; SM00248; ANK; 1.
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InterPro; IPR006638; B1p3.
InterPro; IPR007197; Radical_SAM.
Pfam; PF0210; B12-binding; I.
Pfam; PF04055; Radical_SAM; I.
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EMBL; AE001788; AAD36406.1; -.
PIR; F72265; F72265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54.1%;
53.3%;
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453 LKIRKNVIKIQARVR 467
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Q9C1F2 RESULT 13

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SEQUENCE FROM N.A. Rotian K.-D., Mewes H.W., Lemcke K., Mayer K.F.X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
"Non-Invasive Detection of New Simian Immunodeficiency Virus Lineages in Captive Socty Mangabeys: Ability to Amplify Virion RNA from Fecal Samples Correlates with Plasma Viral Load.";
J. Virol. 0:0-0(2003).

EMBL; AV159611; AA018469.1; -.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0019031; C:viral envelope; IEA.
InterPro; IPR000328; Env GP41.
Pfam; PF00517; GF41; 1.
NON_TER 14 1.
NON_TER 146 AA; 17398 MW; 329A10B9B2435486 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ED Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
L. Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
-1- STMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
REBL; AL021636; CAA46589.1; -.
REBL; AL021636; CAA46589.1; -.
REMBL; AL021636; TO4645.
REMBL; AL0645; TO4645.
REMBL; AL06467; F:protein serine/threonine kinase activity; IEA.
RO; GO:0006474; F:protein amino acid phosphorylation; IEA.
RO; GO:00064674; F:protein amino acid phosphorylation; IEA.
RO; GO:00064674; F:protein amino acid phosphorylation; IEA.
RO; GO:0006679; Protein amino acid phosphorylation; IEA.
RO; RO:0006679; Protein amino acid phosphorylation; IEA.
ROS:0000669; pkinase: 2.
RECOPOM; PRO00001; Prot kinase; 2.
RRODM; PRO0019; PROTEIN KINASE ATP; 1.
RROSITE; PS00107; PROTEIN KINASE ATP; 1.
RROSITE; PS00107; PROTEIN KINASE ST;
RROSITE; PS00108; PROTEIN KINASE ST;
RROSITE; PS00108; PROTEIN KINASE ST;
RROSITE; PS00108; PROTEIN KINASE ST;
RROSITE; PS00109; PROTEIN KINASE ST;
RROSITE; PS00109; PROTEIN KINASE ST;
RROSITE; PS00107; PROTEIN KINASE
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01-JUN-1999 (TrEMBLrel. 09, Last sequence update)
01-OT-2003 (TrEMBLrel. 25, Last annotation update)
Serine/threonine protein kinase like protein.
F10N7.190 OR AT4G32000.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

Terryn N., Ardiles W., Buysshaert C., Dasseville R., De Clerck R.,
De Keyser A., Neyt P., Rouze P., Van Den Daele H., Villaroel R.,
Gielen J., Van Montagu M., Mewes H.W., Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                              52.7%; Score 39; DB 15; Length 146; 40.0%; Pred. No. 43; ive 8; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

Bevan M., Koetter P., Hempel S., Entian K.-D., Hoheisel
Mewes H.W., Mayer K.F.X., Schueller C.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
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129 LRIVIYVVQMSARLR 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 VKVLEYVIKVSARVR 15
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 40.0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pichia angusta (Yeast) (Hansenula polymorpha).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Pichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P. SEQUENCE FACT.

A GADHOLOW M.O., Chechenova M.B., Deev A.V., Packeiser A.N.,
A Ter-Avanesyan M.D.;
Ter-Avanesyan M.D.;
Ter-Avanesyan M.D.;
Ter-Avanesyan M.D.;
Ter-Avanesyan M.D.;
Ter-Avanesyan M.D.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
BMBL; AF339501; AAX26326.1; -...
DR InterPro; IPR001682; Coatomer_WDAD.
DR Pfam; PP004053; Coatomer_WDAD.
DR Pfam; PP004063; Coatomer_WDAD; 1.
DR PF004063; Coatomer_WDAD; 1.
DR PF004063; WD40; 7.
DR PROSTE; PS000018; WD406; 5.
DR PROSITE; PS050082; WD MB40; 5.
DR PROSITE; PS050082; WD_REPEATS_1; 2.
DR PROSITE; PSS50082; WD_REPEATS_REGION; 1.
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                                                                                                                Score 40; DB 16; Length 594;
Pred. No. 1.1e+02;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=SMM.US.-.M922;
Ling B., Santiago M.L., Meleth S., Gormus B., McClure H.M.,
Apetrei C., Hahn B.H., Marx P.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1206 AA; 135629 MW; E6F1212657DBEE14 CRC64;
  SMART; SM00729; Elp3; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 594 AA; 68904 MW; 8D256B90P62BB07A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11723;
                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1206 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Envelope glycoprotein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         572 IKTLENTLYVIKVSGRQCF 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VKVLE---YVIKVSARVRF 16
                                                                                                           54.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 57.99
Matches 11; Conservative
                                                                                                           Query Match
Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                 288 LEYIIKKGGRVR 299
                                                                                                                                                                                                                            4 LEYVIKVSARVR 15
                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
Alpha-COP-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Repeat; WD repeat.
SEQUENCE 1206 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4905;
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Q7 ZRN4 Q7 ZRN4;

RESULT 14

8 셤

Query Match 52.7%; Score 39; DB 10; Length 379; Best Local Similarity 66.7%; Pred. No. 1.18+02; Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

1 VKVLEYVIKVSA 12 | | | | | :: | | | | 14 VSVLEFIISVSA 25

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Db 14 VSVLEFIISVSA 25

Search completed: October 7, 2004, 15:16:57 Job time: 60.8182 secs

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; Search time 62.9091 Seconds (without alignments) 71.862 Million cell updates/sec
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version 5.1.6 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                        1586107 segs, 282547505 residues
                                                            - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                       US-09-336-091-4
80
1 EYVIKVSARVRFFFPS 16
GenCore
Copyright (c) 1993
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Sequence:
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Maximum DB
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2003as:\* geneseqp2003bs:\*

geneseqp2004s:\*

geneseqp2002s:\* geneseqp2001s:\*

geneseqp1980s:\* geneseqp1990s:\* geneseqp2000s:\* A\_Geneseq\_29Jan04:\*

Database

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Degnit		* 6			SUMMARIES	
No.	Score	Match	Length DB	80	DI	Description
-	80	100.0	16	4	AAB31292	
8	80	100.0	30	Ŋ	AAU85042	Aau85042 Human MAG
е	80	100.0	309	~	AAR70909	Aar70909 Human mel
4	80	100.0	309	~	AAW81548	Aaw81548 Tumour re
S	80	100.0	309	4	AAB31290	Aab31290 Amino aci
9	80	100.0	309	4	AAE06806	Aae06806 Human MAG
7	80	100.0	309	ഹ	AAU84814	Aau84814 Human MAG
80	80	100.0	309	ø	ABP74195	Abp74195 Human MAG
σ	80	100.0	309	9	ABU08930	Abu08930 Human tum
10	80	100.0	309	7	ADC09573	Adc09573 MAGE-1 pr
11	80	100.0	310	9	AA019742	Aao19742 Wild-type
12	80	100.0	316	9	ABU04419	Abu04419 Human exp
13	80	100.0	445	~	AAY06592	_
14	80	100.0	446	~	AAY06590	Aay06590 Lipoprote
15	80	100.0	1052	9	ABR57354	_
16	80	100.0	3541	ß	AAU85130	Aau85130 Human mel
17	64	80.0	28	ហ	AAU85043	Aau85043 Human MAG
18	9	75.0	12	4	AAB31296	Aab31296 Peptide d
19	57	71.2	12	4	AAB31295	Aab31295 Peptide d
20	57	71.2	16	4	AAB31291	Aab31291 Peptide d
21	51	63.7	317	~	AAY06998	Aay06998 MAGE-4 pr
22	51	63.7	317	9	ABU56545	Abu56545 Lung canc
23	51	63.7	317	9	ADA83770	Ada83770 Human MAG
24	51	63.7	318	m	AAB08734	Aab08734 Amino aci
25	49	61.3	10	7	AAR70951	Aar70951 Human mel

	Aay38326 MAGE-deri Aar70948 Human mel	Aar70960 Human mel	Aay46118 Immunogen	Aay45907 Immunogen	Abp74245 Human MAG	Adc09104 Epitope w	Aar70953 Human mel	Aay46179 Immunogen	Aar70933 Human mel	Aay46137 Immunogen	Aar70927 Human mel	Aar70921 Human mel	Aay46136 Immunogen	Aay47262 Immunogen	Aay92316 MAGE-Al a	Aay92274 MAGE-A1 a	Aae31182 Human mag
AAB31301	AAY38326 AAR70948	AAR70960	AAY46118	AAY45907	ABP74245	ADC09104	AAR70953	AAY46179	AAR70933	AAY46137	AAR70927	AAR70921	AAY46136	AAY47262	AAY92316	AAY92274	AAE31182
10 2	10 10 2	10 2	10 2	10 2	10 6	10 7	10 2	10 2	9	9	9	9	9	9	9	9	9
49 61.3	46 57.5 46 57.5	46 57.5	46 57.5	46 57.5	46 57.5	46 57.5	45 56.2	45 56.2	44 55.0	44 55.0	43 53.8	43 53.8	43 53.8	43 53.8	43 53.8	43 53.8	43 53.8
26 27	7 7 8 7 8	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

Novel MAGE-A1 human leukocyte antigen class II peptides which bind to and are presented to the class II molecules, useful for inducing immune response and treating cancers characterized by expression of MAGE-A1. Van Der Bruggen P; MAGE-A1; HLA; human leukocyte antigen; CD4+ T lymphocyte; cancer; MAGE-A1 HLA class II-binding protein; vaccine. Peptide derived from human MAGE-Al HLA class II-binding protein. Boon-Falleur T, Æ Chaux P, Claim 3; Page 42; 78pp; English. AAB31292 standard; peptide; 16 (LUDW-) LUDWIG INST CANCER RES. 14-JUN-2000; 2000WO-US016287. 99US-00336091. (first entry) Van Snick J, Lethe B, WPI; 2001-102698/11. WO200078806-A1. Homo sapiens. 18-JUN-1999; 20-APR-2001 28-DEC-2000. AAB31292; RESULT 1 AAB31292 

The present sequence is derived from a human MAGE-A1 HLA (human leukocyte antigen) class II-binding protein. Peptides derived from the MAGE-A1 HLA binding protein stimulate the activity and proliferation of CD4+ T lymphocytes. The MAGE-A1 HLA binding protein is useful as a diagnostic agent for diagnosing a disorder characterized by expression of MAGE-A1. The protein is used for treating a disorder characterized by expression of MAGE-A1 such as cancers e.g. melanomal, squamous cell carcinomas, colorectal carcinomas, osteosarcomas, and lymphocytic leukemias. Peptides derived from the MAGE-A1 HLA binding protein are useful in the production of anti-tumour vaccines

Sequence 16 AA;

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The invention relates to a new synthetic polypeptide (I) comprising several different segments of at least one parent polypeptide linked together in a different relationship relative to their linked of parent polypeptide to impede, abrogate or otherwise alter at least one function associated with the parent polypeptide and for inducing an immune response against a pathogen or cancer. Also included are a synthetic polypeptides. The synthetic polypeptides and polymotleotide encoding and a computer system for designing the synthetic polypeptides. The synthetic polypeptides and polymotleotides are referred to as a Savine. The synthetic polypeptide is useful for modulating immune responses preferably directed against a pathogen or a cancer, (e.g., cancers of the lung, breat, ovary, cervix, colon, head on neck, pancreas, prostate, stomach, bladder, kidney, bone liver, and neck, pancreas, prostate, stomach, bladder, kidney, bone liver, compositions comprising the polypeptide may be used in the treatment or prophylaxis against viral (such as infections caused by HIV (human immunity, Epstein-Barr virus, betaind respiratory syncytial virus), bacterial (e.g., infections caused by Neisseria, Meningococcal, Haemophilus, Slamonella, Streptococcal, Legionella and Mycobacterium or parasitic (e.g., infections caused by Neisseria, Meningococcal, Haemophilus, Trypanosoma, Toxoplasma and Glazdia) infections. The present sequence is a peptide derived from a parent protein used to construct a savine of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New synthetic polypeptides having several different segments of at least one parent polypeptide linked together differently compared to the linkage in the parent polypeptide, for inducing immune response against a
                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                              Savine, vaccine; cancer, viral infection, HIV, hepatitis C virus, viral infection; human immunodeficieny virus; melanoma; bacterial infection; Salmonella, Legionella; parasitic infection,
                                             ö
      Length 16;
                                           Indels
    Score 80; DB 4; L
Pred. No. 6.5e-08;
; Mismatches 0;
                                                                                                                                                                                                                       AAU85042 standard; peptide; 30 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Trypanosoma; Toxoplasma; Giardia
                                           ö
    100.0%;
                                                                               1 EYVIKVSARVRFFFPS 16
                                                                                                                      EYVIKVSARVRFFFPS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAY-2001; 2001WO-AU000622
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                                                                                                                                                                                                                                                                                                  (first entry)
Query Match
Best Local Similarity 100.
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                       Human MAGE-1 segment 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-147575/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pathogen or cancer.
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                                                                                                                                                                                                                                                              AAU85042;
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Sequence 30 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQ85435 encodes AAR70909 human melanoma antigen MAGE-1, it was used to produce the C-terminal MAGE-1 peptides described in AAR70915 to AAR70969. These peptides are useful for defining epitopes that engender a HLA-restricted cytotoxic lymphocyte activity against MAGE-1 antigens. Compans. containing these peptides can be administered, as a vaccine to patients susceptable to MAGE associated tumours, e.g. melanomas. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human melanoma antigen, MAGE-1, peptide(s) - useful for stimulating immune response against melanoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human melanoma antigen; MAGE-1; vaccines; MAGE associated tumours; HLA-restricted cytotoxic T-lymphocyte activity.
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                          Length 30
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                                                                                 0; Indels
                          Score 80; DB 5;
Pred. No. 1.3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sidney JC,
                                                                              Mismatches
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                       100.0%; Sc
100.0%; Pr
:ive 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human melanoma antigen MAGE-1.
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                                                                                                                                         16
                                                                                                                                                                         13 EYVIKVSARVRFFFPS 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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Query Match
Best Local Similarity 100..
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les 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1995-090681/12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               25-MAR-2003
09-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-FEB-1995.
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This is the amino acid sequence of human tumour rejection antigen precursor (TRAP) MAGE-A1 CDNA (see AAV69719) shows homology to movel human MAGE-C1 cDNA (see AAV69720). MAGE-C1 (see AAW81546) is a novel member of the MAGE family that may be recognised by cytotoxic T cells, leading to lysis of the tumour cells which express it. It is expressed in a variety of tumours and in normal testis cells, but not by other normal cells. The invention provides MACE-C1 and MACE-C2 nucleic acids and polypeptides, useful e.g. in a claimed method for determining the presence of cytolytic T cells specific for complexes of a human
                                                                                                                                                                                                                                                                                                                       rejection antigen precursors - used for determining presence of tic T cells specific for complexes of a human leukocyte antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                              tumour rejection antigen precursor; TRAP; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amino acid sequence of human MAGE-Al HLA class II-binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAGE-A1; HLA; human leukocyte antigen; CD4+ T lymphocyte; cancer; MAGE-A1 HLA class II-binding protein; vaccine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 80; DB 2; Length 309; 100.0%; Pred. No. 1.8e-06; ive 0; Mismatches 0; Indels
 Tumour rejection antigen precursor MAGE-Al.
                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 50-51; 84pp; English.
                                                                                                                                                                                                                                                Boon-Falleur T;
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                                                                                                                                                                                                                   (LUDW-) LUDWIG INST CANCER
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Best Local Similarity 100.
Matches 16, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             leukocyte antigen (HLA)
                                                                                                                                                                                                                                                De Smet C,
                                                                                                                                                                                                                                                                             WPI; 1999-024041/02.
                                                                                                                                                                                                                                                                                          N-PSDB; AAV69719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 309 AA;
                           MAGE-Al; human;
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                                                                                                                                                          24-APR-1998;
                                                                                                                                                                                       25-APR-1997;
                                                                       Homo sapiens
                                                                                                  WO9849184-A1
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                                                                                                                               05-NOV-1998.
                                           diagnosis.
                                                                                                                                                                                                                                                                                                                                      cytolytic
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                                                                                                                                                                                                                                                Lucas S,
                                                                                                                                                                                                                                                                                                                       Tumour
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                                                                                           Novel MAGE-A1 human leukocyte antigen class II peptides which bind to and are presented to the class II molecules, useful for inducing immune response and treating cancers characterized by expression of MAGE-A1.
                                                                                                                                                                                                     antigen) class II-binding protein. Paptides derived from the MAGE-AI HLA binding protein stimulate the activity and proliferation of CD4+ T lymphocytes. The MAGE-AI HLA binding protein is useful as a diagnostic agent for diagnosing a disorder characterized by expression of MAGE-AI. The protein is used for treating a disorder characterized by expression of MAGE-AI such as cancers e.g. melanomal, squamous cell carcinomas, colorectal carcinomas, osteoastcomas, and lymphocytic leukemias. Peptides derived from the MAGE-AI HLA binding protein are useful in the production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Functional variants and isolated mimetics of a MAGE-A1 HLA-B35 or HLA-B44 binding peptide, used in diagnosis and treatment of a disorder characterized by expression of MAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAGE antigenic peptide; Human leukocyte antigen; HLA-B35; HLA-B44; tumour cell; immunostimulant; antigen presentation; cancer; melanoma; CD8+ cytotoxic T lymphocyte; colorectal; prostate; gastric carcinoma; myeloma; brain tumour; sarcoma; seminoma; ovarian tumour; cytostatic; gene therapy; human; MAGE-A1; tumour rejection antigen; TRA.
                Van Der Bruggen P;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                         represents a human MAGE-Al HLA (human leukocyte
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                                                                                                                                                                                                                                                                                                                                                                                                       Length 309;
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               Boon-Falleur T,
                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 80; DB 4; 1 100.0%; Pred. No. 1.8e-06;
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                Chaux P,
                                                                                                                                                           Claim 1; Page 63; 78pp; English.
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25-OCT-2000; 2000US-0243212P.
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Best Local Similarity 100.
Marches 16; Conservative
                                                                                                                                                                                                                                                                                                                                            of anti-tumour vaccines
                Lethe B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human MAGE-Al protein.
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                                               WPI; 2001-102698/11.
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                                                                 N-PSDB; AAF24676
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                /an Snick J,
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Demotte N,
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(LUDW-) LUDWIG INST CANCER RES

99US-00336091

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14-JUN-2000; 2000WO-US016287

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                                          The invention relates to functional variants and isolated mimetics of a MAGE-A1 human leukocyte antigen (HLA)-B35 or HLA-B44 binding peptide, or of a MAGE-A3 HLA-B35 binding peptide, identified by methods described in the specification. MAGE genes encode tumour rejection antigens (TRAs) presented to T lymphocytes by HLA-B35 and HLA-B44 molecules. The MAGE antigenic peptide acts by binding to HLA molecules on tumour cells and elimulating recognition of these cells and thus signalling them to the immune system for destruction. The peptide when presented by HLA molecule induces the activation and stimulation of CD8+ cytocoxic T lymphocytes. The MAGE antigenic peptide is used to treat and diagnose disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New synthetic polypeptides having several different segments of at least one parent polypeptide linked together differently compared to the linkage in the parent polypeptide, for inducing immune response against a pathogen or cancer.
                                                                                                                                                                                                        characterised by expression of MAGE-Al or -Al. Disorders include cancers e.g melanomas, oesophageal, lung, head and neck, breast, colorectal, prostate, renal, bladder, hepatocellular, papillary thyroid and gastric carcinomas, myelomas, brain tumours, sarcomas, seminomas, and ovarian tumours. The present sequence is human MAGE-Al protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a new synthetic polypeptide (I) comprising several different segments of at least one parent polypeptide linked together in a different relationship relative to their linkage in the parent polypeptide to impede, abrogate or otherwise alter at least one function associated with the parent polypeptide and for inducing an
                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                          Length 309;
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Pred. No. 1.8e-06;
; Mismatches 0;
             Claim 2; Page 86-87; 103pp; English.
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Best Local Similarity 100.0
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                          Sequence 309 AA;
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immune response against a pathogen or cancer. Also included are a synthetic polypeptides encoding and a computer system for designing the synthetic polypeptides. The synthetic polypeptides and polynucleotides are referred to as a Savine. The synthetic polypeptide is useful for modulating immune responses preferably directed against a pathogen or a cancer, (e.g., cancers of the lung, breast, ovary, cervix, colon, head and neck, pancrass, prostate, stoomach, bladder, kidney, borne liver, cospopagus, brain, testicle, uterus), as potentiating agents. Compositions comprising the polypeptide may be used in the treatment or prophylaxis against virus), hepatitis, influenza, Japanese encephalitis virus, Epstein-Barr virus and respiratory syncytial virus), bacterial (e.g., infections caused by Neisseria, Meningococcal, Haemophilus, Salmonella, Streptococcal, Legionella and Mycobacterium or paragitic (e.g., infections caused by Plasmodium, Schistosoma, Leishmania, Trypanosoma, Toxoplasma and Gladdia) infections. The present sequence is a consensus sequence for a parent protein used to design a savine of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; epitope; vaccine; immunotherapeutic; cytostatic; immunogenicity;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel epitopes useful as vaccines, comprises peptides or nucleic acid encoding the peptides, that are useful epitopes of target-associated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 309 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                   invention
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polynucleotide sequence. Also disclosed is a method which is useful for determining presence of cytolytic T-cells specific for complexes of human leukocyte antigen (HLA) and a peptide detrived from the nucleic acid in a cytocoxic T-lymphocyte (CTL)-containing sample. The nucleic acid is useful as a diagnostic probe to determine the presence of abnormal
immunogenicity of a vaccine or immunotherapeutic composition, by administering VC to an HIA-transgenic animal and evaluating immunogenicity based on a characteristic of the animal, or by in vitro primary stimulation of a T cell and evaluating immunogenicity. (I) is useful for determining specific T cell frequency, by contacting T cells with a MHC-peptide complex, and further comprises ELISPOT analysis, limiting dilution analysis, flow cytometry, in situ hybridisation and/or polymerase chain reaction (PRR). ABQ83843 to ABQ83858 and ABP74128 to ABP74111 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRAP; tumour rejection antigen precursor; cytolytic T-cell; CTL; tumour; seminoma; NSCLC; adaptor; head-and-neck squamous-cell carcinoma; breast carcinoma; sarcoma; cutaneous melanoma; nonsmall cell lung cancer; MAGE-A1; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated nucleic acid encoding tumor rejection antigen precursor MAGE-C3, MAGE-B5, or MAGE-B6, useful as diagnostic probes to determine presence of abnormal e.g., tumor cells expressing MAGE-C1, MAGE-B5 or
                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                      100.0%; Score 80; DB 6; Length 309; 100.0%; Pred. No. 1.8e-06;
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17-DEC-1999; 99US-00468433.
09-FEB-2000; 2000US-00501104.
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(BOON/) BOON-FALLEUR T.
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                                                                                                                                                                                                   Sequence 309 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US2002176865-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-NOV-2002
                                                                                                                                                                   invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABU08930;
                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lucas S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAGE-B6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human
                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                      ABU08930
     888888888888888
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           head-and-neck squamous-cell carcinoma, breast carcinoma, sarcoma, cutaneous melanoma or nonsmall cell lung cancer (NSCLC) which express MAGE-C1, MAGE-B5 or MAGE-B6. The nucleic acid is useful for diagnosing a disorder characterised by expression of MAGE-C1, MAGE-B5 or MAGE-B6 TRAPs or tumour rejection antigens (TRAs). The present sequence represents the amino acid sequence of the human tumour rejection antigen MAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          class I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Epitope having high affinity for major histocompatibility complex class : useful for treating an animal, evaluating immunogenicity of a vaccine or
                                                                                                                                                                                                                                     Gaps
(tumour) cells such as seminoma, bladder transitional-cell carcinoma,
                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Epitope; immunological; vaccine;
major histocompatibility complex class I; WHC class I; cancer;
                                                                                                                                                                                                 100.0%; Score 80; DB 6; Length 309; 100.0%; Pred. No. 1.8e-06;
                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          therapeutic composition and for diagnosing a disease.
                                                                                                                                                                                                                                     0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 71; 239pp; English
                                                                                                                                                                                                                                                                                                                                                                                                   ADC09573 standard; protein; 309 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CTLI-) CTL IMMUNOTHERAPIES CORP.
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                                                                                                                                                                                                                                                                                                         296
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2002US-0363210P.
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                                                                                                                                                                          Query Match
Beet Local Similarity 100.v.
The 16; Conservative
                                                                                                                                                                                                                                                                                              281 EYVIKVSARVRFFFPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                       1 EYVIKVSARVRFFFPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAGE-1 protein #SEQ ID 71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diamond DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-248010/24.
                                                                                                                                                             Sequence 309 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2003008537-A2.
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07-MAR-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Simard JJL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JAN-2003
                                                                                                                                                                                                                                                                                                                                                               RESULT 10
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Translational profiling, expressed protein tag; EPT; kinase; phosphatase; protease; protease inhibitor; transporter; cytoskeletal protein; receptor; transcription factor; cancer; WHC; major histocompatability complex; myeloma; colon cancer; gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polypeptides (e.g. kinases, phosphatases, proteases, transporters, cytoskeletal proteins, receptors or transcription factors), useful for treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or leukemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; SEQ ID NO 1085; 134pp; English.
                                                                                                         Human expressed protein tag (EPT) #1085.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Urban RG;
 ABU04419 standard; protein; 316
                                                                                                                                                                                                                                                                                                                                                                                                28-WAR-2001; 2001US-0279495P.
21-WAY-2001; 2001US-0292544P.
08-4WG-2001; 2001US-0310801P.
01-0CT-2001; 2001US-0336780P.
04-DEC-2001; 2001US-0336780P.
                                                                                                                                                                                                                                                                                                                                                                28-MAR-2002; 2002WO-US009671.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-FEB-2002; 2002US-0358985P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EYVIKVSARVRFFFPS 16
                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tomlinson AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-040607/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ZYCO-) ZYCOS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 316 AA;
                                                                                                                                                                                                                                                                                           WO200278524-A2
                                                                                                                                                                                                                                                         Homo sapiens.
                                                                       29-JAN-2003
                                                                                                                                                                                                                                                                                                                             10-OCT-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chicz RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a pharmaceutical composition containing at least one modified RNA encoding a biologically active or antigenic protein. The RNA is modified to optimise translation of the sequence. The compositions are used for vaccination against a wide range of infectious diseases (viral, bacterial or protozoal) or cancer, or for tissue regeneration, e.g. in cases of Alzheimer's or Parkinson's diseases and arthritis, but also to express proteins such as dystrophins, chloride ion channels (for treating cystic fibrosis) and enzymes (either for treating metabolic disorders or for synthesis of neurotransmitters such as
                                                                                                                                                                                                                                                                                                                                                                              Stabilised mRNA; translation optimised; vaccine; tissue repair; sequence modification determination; gene therapy; cytostatic; virucide; antibacterial; protozoacide; nootropic; neuroprotective; infection; antiparkinsonian; immunostimulant; cancer; MAGBI protein.
                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Composition containing mRNA modified for optimal translation and stability, useful for treating e.g. tumors or infections, comprises increased G/C content and fewer rare codons.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 80; DB 6; Length 310; 100.0%; Pred. No. 1.8e-06;
                                 100.0%; Score 80; DB 7; Length 309; 100.0%; Pred. No. 1.8e-06;
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                                                                     Indels
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                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pascolo S;
                                                                                                                                                                                                                                     AAO19742 standard; protein; 310 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 2B; 75pp; German.
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0
                                                                                                                               EYVIKVSARVRFFFPS 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUN-2001; 2001DE-01027283
                                                                                                       1 EYVIKVSARVRFFFPS 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Von Der Muelbe F, Hoerr I,
                                                                                                                                                                                                                                                                                                          (first entry)
                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (VMUE/) VON DER MUELBE F
                                                                                                                                                                                                                                                                                                                                            Wild-type MAGE1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-148621/14.
                                                  Best Local Similarity
Matches 16; Conserv
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Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ABZ69107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 310 AA;
Sequence 309 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200298443-A2.
                                                                                                                                                                                                                                                                                                          11-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-DEC-2002
                                                                                                                                                                                                                                                                      AA019742;
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                                   Query Match
                                                                     Matches
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fragment of a kinase, phosphatase, protease, which comprises a fragment of a kinase, phosphatase, protease, protease inhibitor, camporter, cytoskeletal protein, receptor or transcription factor. The polypeptide is useful as an immunogenic composition for eliciting in a mammal an immunogenic response directed against any of the purified polypeptide, or the antibody that binds to this polypeptide. The purified polypeptide, or the antibody that binds to this polypeptide, is useful for treating cancer. The polypeptide is also useful for treating compounds that binds to a naturally processed class I or class II MHC-binding polypeptide. The polypeptides and colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, lymphoma or leukaemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an expressed protein tag (EPT) isolated from human tissue for translational profiling. Note: This sequence does not appear in the printed promitived specification but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 80; DB 6; Length 316; 100.0%; Pred. No. 1.8e-06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   288 EYVIKVSARVRFFFPS 303
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RESULT 13 AAY06592

RESULT 12 ABU04419

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The present sequence represents a novel fusion protein composed of lipidated protein D (LPD) of Haemophilus influenzae B, the human MAGE-1 tumour-associated antigen and a hexahistidine tail. The invention relates to MAGE proteins fused to an immunological fusion partner such as LPD. The LPD moiety provides the fusion protein with additional exogenous T-call epitopes and also increase expression levels in E. coli. The lipid tail ensures optimal presentation of the antigen to antigen-presenting cells. The affinity tag facilitates purification. The novel fusion proteins provide vaccines for immunocherapy of melanomas or other MAGE-associated tumours like breast, bladder, lung and non-small cell lung cancer, head and squamous cell carcinoma, colon carcinoma and oesophagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New protein derivatives used in cancer vaccine therapy for treating a range of cancers including melanomas, carcinomas and cancers of breast.
                        head and squamous cell carcinoma; colon cancer; oesophagus carcinoma; vaccine; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antigen presenting cell; vaccination; nootropic; neuroprotective; antiatrentosclerotic; cytostatic; antidiabetic; heptotropic; antiation antianisheric; tengoics; antibacterial; virucide; vaccine; Alzheimer's disease; atherosclerosis; cancer; diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 80; DB 2; Length 446; 100.0%; Pred. No. 2.7e-06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cabezon Silva T, Cohen J, Slaoui MM, Vinals Bassols C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MatDC16-C-gamma-4-MAGE-Al amino acid sequence.
breast cancer; bladder cancer; lung cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                    (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 6; Page 67-68; 72pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   409 EYVIKVSARVRFFFPS 424
                                                                                                                                                                                                                                                                                                                 99WO-EP000660.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 16; Conservative
                                                                                              Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hepatitis; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-494293/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAX87591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 446 AA;
                                                                                                                       Homo sapiens.
Synthetic.
                                                                                                                                                                                                                WO9940188-A2
                                                                                                                                                                                                                                                                                                                 02-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                              05-FEB-1998;
06-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABR57354;
                                                                                                                                                                      Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
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  SON COURT OF THE STANDARD STAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a fusion protein composed of the C-terminal portion of the Streptococcus pneumoniae LYTA protein (CLYTA), the human MAGE-1 tumour-sesociated antigen and a hexahistidine tail. A vector designed for recombinant expression of the fusion protein in soluble fusion protein. Acciliates affinity purification, and also acts as a T-helper epitope. The invention relates to MAGE proteins fused to an immunological fusion partner, e.g. CLYTA-MAGE-1-His. These novel fusion proteins provide vaccines for immunocherapy of melanomas or other MAGE-associated tumours like breast, bladder, lung and non-small cell lung cancer, head and squamous cell carcinoma, colon carcinoma and oesophagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAGE-1; lipoprotein D; LPD-MAGE-1-His; fusion protein; tumour; melanoma;
                                                                                                                                                                                        MAGE-1; CLYTA-MAGE-1-His; fusion protein; tumour; melanoma;
breast cancer; bladder cancer; lung cancer; colon cancer;
head and squamous cell carcinoma; oesophagus carcinoma; vaccine; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New protein derivatives used in cancer vaccine therapy for treating a range of cancers including melanomas, carcinomas and cancers of breast.
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  AAY06592 standard; protein; 445
                                                                                                                                           CLYTA-MAGE-1-His fusion protein.
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                                                                                                                                                                                                                                                                                      Streptococcus pneumoniae.
Homo sapiens.
Synthetic.
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The present invention describes a conjugate (I) for targeting antigen conjugated to a targeting moiety that is capable of binding to a cell conjugated to a targeting moiety that is capable of binding to a cell surface structure of an APC, and upon binding, inducing a cytotoxic T (I ymphocyte (CTL) and T-halper response. Also described: (I) a nucleic conjugated to expression sequence, operably linked of expression sequences for the APC; (3) a host cell transformed or transfected using the nucleic acid or expression vector; (4) a method for producing (I); (5) a method for generating an APC, capable of eliciting an immune response via MHC classes I and II presentation of processed antigen fragments; and (6) a pharmaceutical composition comprising (I) or the APC. (I) has nootropic, neuroprotective, virucide, antianteriosclerotic, cytostatic, antidabetic, hepatotropic, fungicide, antianteriosclerotic, Alzheimer's disease, atherosclerosis, and can be used in vaccines. The conjugate (I) or APC can be used for preventing, cancer, diabetes, hepatitis or paramitic, fungal, bacterial or viral infections. The present sequence represents a MatDC16-C-gamma-4-MAGE-AI infections. The present sequence represents a MatDC16-C-gamma-4-MAGE-AI invaniants.
                                                                                                                                                                                                                                                                                                                                                           New conjugate for targeting antigen presenting cells, useful for preventing, retardating or treating e.g., Alzheimer's disease, atherosclerosis, cancer, diabetes, hepatitis or fungal, bacterial or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 80; DB 6; Length 1052; 100.0%; Pred. No. 6.9e-06; tive 0; Mismatches 0; Indels (
                       /note= "unspecified"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 2; 54pp; English.
                                                                                                                                                                                          30-NOV-2001; 2001WO-EP014255
                                                                                                                                                 30-NOV-2001; 2001WO-EP014255
                                                                                                                                                                                                                                  (CRUC-) CRUCELL HOLLAND BV.
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Misc-difference 546
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                                                               WO2003046011-A1
                                                                                                                                                                                                                                                                             Germeraad W;
                                                                                                        05-JUN-2003
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Gaps ; 0

> 7, 2004, 15:13:02 Search completed: October Job time : 63.9091 secs

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Scoring table:

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Query Match 100.0%; Score 80; DB 1; Length 58; Best Local Similarity 100.0%; Pred. No. 2.7e-07; Matches 16; Conservative 0; Mismatches 0; Indels
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APPLICANT: Livingston, Brian D.
APPLICANT: Sette, Alessandro D.
APPLICANT: State, Alessandro D.
APPLICANT: State, Alessandro D.
APPLICANT: State, Alessandro D.
APPLICANT: State, Alessandro D.
TITLE OF INVENTION: INMUNOGENIC PEPTIDES (as amended)
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
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ZIP: SAID
COUNTRY: USA
ZIP: 98111
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAPLICATION DATA:
APPLICATION NUMBER: US/08/465,167A
FLING DATE: 05-JUN-1995
CLASSIFICATION NUMBER: US/08/465,167A
FLING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAMME: PARMELSE, US 08/103,623
ATTORNEY/AGENT INFORMATION:
NAMME: PARMELSE, 1933
ATTORNEY/AGENT INFORMATION:
NAMME: PARMELSE, 1930
REFERENCE/DOCKET NUMBER: 14137-60-1
TELECOMMUNICATION NUMBER: 14137-60-1
                              PCT-US95-02121-152
US-09-328-352-5371
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US-09-489-039A-7753
US-09-540-236-3375
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US-09-465-167A-39
US-09-403-667A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 1, Application US/08465167A; Patent No. 5750395; GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 58 aming Truence: 1.
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                                       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-465-167A-46

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US-08-627-820-8
US-09-543-608A-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -08-197-484-93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                       - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Issued Patents AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq length: 0 seq length: 2000000000
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80
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Match Length
                                                                                                                                                                                                                                                                                               October
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Score

Result Š. ö

Gaps

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RESULT 4
US-08-993-118-10
i Sequence 10, Application US/08993118
i Sequence 10, Application US/08993118
i Patent No. 5997872
i GENERAL INFORMATION:
APPLICANT: LUCAS, Sophie;
APPLICANT: BOS FALIEUR, Thierry
APPLICANT: BOS FALIEUR, Thierry
TITLE OF INVENTION: REJECTION ANTIGEN PRECURSOR MAGE-C1 AND USES
ITILE OF INVENTION: THEREOF
ITILE OF INVENTION: THEREOF
CORRESPONDENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 80; DB 1; Length 309; 100.0%; Pred. No. 1.7e-06; tive 0; Mismatches 0; Indels
          IMMUNOGENIC PEPTIDES (as amended)
                                                                                                                                                                                                                                                                                                                                COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,167A
FILING DATE: US-JUN-1995
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/103,623
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: PATMELS, SEEVEN W.
REGISTRATION NUMBER: 31,990
REGISTRATION NUMBER: 31,990
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                         Townsend and Crew LLP
Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 36(
COMPUTER: 1BM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,118
PILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORRESEE: Felfe & Lyc. ADDRESSEE: Felfe & Lyc. STREET: 805 Third Avenue CITY: New York City STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 24: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 281 EYVIKVSARVRFFFPS 296
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and TC
STREET: Two Embarcadero Ce
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EYVIKVSARVRFFFPS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 309 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             415-576-0300
                                                                                                                                                                                                                                                               ZIP: 98111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
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USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
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                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF THE
COMPLETE MAGE 1 GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTY: U.S.A.

ZIP: 94105
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: BAPC COMPACIBLE
COMPUTER: BAPC COMPACIBLE
COMPUTER: PC-DOS/MS-DOS
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCATION DATA:
APPLICATION NUMBER: US/08/627,820
FILING DATE: 02-Apr-1996
CLASSIFICATION: CURKOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/103,623
FILING DATE: CURKOWN>
ATTORNEY/AGENT INFORMATION:
NAME: DATE: CURKIOWN:
ATTORNEY/AGENT INFORMATION:
NAME: CONTROLLED CALORION CONTROLLED CONTROLLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSES: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 80; DB 4; Length 58; 100.0%; Pred. No. 2.7e-07;
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US-08-465-167A-24
; Sequence 24, Application US/08465167A
; Patent No. 7550395
; GENERAL INFORMATION:
; APPLICANT: Fikes, John D.
; APPLICANT: Sette, Alessandro D.
; APPLICANT: Sette, Alessandro D.
; APPLICANT: Stoney, John C.
; TITLE OF INVENTION: DNA ENCODING MAGE-1 C-TERMINAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-60
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
TELEPAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Fikes, John D.
Livingston, Brian D.
Sette, Alessandro D.
                                                                                                                                                                                                                                                                   Sequence 1, Application US/08627820
Patent No. 6464980
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
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                                                                                        30 EYVIKVSARVRFFFPS 45
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                                            1 EYVIKVSARVRFFFPS 16
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Best Local Similarity
Matches 16; Conservat
                                                                                                                                                                                                            RESULT 2
US-08-627-820-1
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Gaps

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Sequence 10, Application US/09066281B
Patent No. 6475730:
Patent No. 6475730:
GENERAL INFORMATION:
APPLICANT: LUCAS, Sophie; DE SMET, Charles; BOON-FALLEUR, Thierry
TITLE OF INVENTION: FOR TUMOR REJECTION ANTIGEN PRECURSOR MAGE-C1 AND MAGE-C2
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
           Gaps
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                                                                                                                                                                                                                                                                                                                                    Sidney, John C.
TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF THE COMPLETE MAGE 1 GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Street Tower CITY: San Francisco
         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,820
FILING DATE: 02-Apr-1996
CLASSIFICATION: <UNKNOWN>
           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 80; DB 4; 1
100.0%; Pred. No. 1.7e-06;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/103,623
FILING DATE: -Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: PATTICLE, Steven W.
REGISTRATION NUMBER: 31,990
TEBERENCE/DOCKET NUMBER: 14137-60
TELECOMMUNICATION INFORMATION:
           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
                                                                                                                                                                                                     Sequence 24, Application US/08627820
Patent No. 6464980
GENERAL INFORMATION:
APPLICANT: Fikes, John D.
Livingston, Brian D.
Sette, Alessandro D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (206) 467-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 309 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (415) 543-5043
                                                                          281 EYVIKVSARVRFFFPS 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (415) 543-51
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
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                                                       16
                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 24
                                                     1 EYVIKVSARVRFFFPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.'
Matches 16; Conservative
           16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-066-281B-10
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           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE CODING FOR TUN
TITLE OF INVENTION: REJECTION ANTIGEN PRECURSOR MAGE-C1 AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 80; DB 2; I
100.0%; Pred. No. 1.7e-06;
Live 0; Mismatches 0;
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
PILING DATE: US/08/845,528
FILING DATE: April 25, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mary Anne Schofield
REGISTATION NUMBER: 36,669
REFERENCE/DOCKET NUMBER: LUD 5455
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 688-9200
TELEPAC: (212) 838-3884
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: 1BM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,528C
FILING DATE: April 25, 1997
CLASSIFICATION: 4335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10, Application US/08845528C
Patent No. 6027924
GENERAL INFORMATION:
APPLICANT: LUCAS, Sophie;
APPLICANT: DE SWET, Charles;
APPLICANT: BOON-FALLEUR, Thierry
                                                                                                                                                                                                                                                                                                             TYPE: amino acids
STRANDEDNESS: single stranded
TOPOLOGY: linear
US-08-993-118-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acids
STRANDEDNESS: single stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Mary Anne Schofield
REGISTRATION NUMBER: 36.669
REFERENCE/DOCKET NUMBER: LUT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     281 EYVIKVSARVRFFFPS 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EYVIKVSARVRFFFPS 16
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: .309
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Best Local Similarity
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US-08-845-528C-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-392-714-29

US-09-392-714-29

Sequence 29, Application US/09392714A

Patent No. 6686147

GENERAL INFORMATION:

APPLICANT: Scanlan, Matthew J.

APPLICANT: Gure, Ali O.

APPLICANT: Williamson, Barbara

APPLICANT: Chen, Yao-Teeng

APPLICANT: Old, Lloyd J.

TITLE OF INVENTION: Therefor

TITLE OF INVENTION: Therefor

TITLE OF INVENTION: Therefor

TITLE OF INVENTION: Therefor

CURRENT APPLICATION NUMBER: US/09/392,714A

CURRENT PILING DATE: 1999-09-09

EARLIER APPLICATION NUMBER: PCT/US98/14679

EARLIER PILING DATE: 1999-07-15

NUMBER OF SEQ ID NOS: 30

SOUTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 29

ITYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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Patent No. 5750395
GENERAL INFORMATION:
APPLICANT: Fikes, John D.
APPLICANT: Sette, Alessandro D.
APPLICANT: Sette, Alessandro D.
APPLICANT: Sidney, John C.
TITLE OF INVENTION: DAM ENCODING MAGE-1 C-TERMINAL
TITLE OF INVENTION: IMMUNOGENIC PEPTIDES (as amended)
NUMBER OF SEQUENCES: 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 80; DB 4; L
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 16; Conservative 0; Mismatches 0;
  PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/845,528
FILING DATE: APAIL 25, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mary Anne Schofield
REGISTRATION NUMBER: 36,669
REFERENCE/DOCKET NUMBER: LUD 5611 JEL/WAS
TELEPHONE: (202) 662-0200
TELEPHONE: (202) 662-0200
TELEPHONE: (202) 662-4643
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                              TYPE: amino acids
STRANDEDNESS: single stranded
TOPOLOGY: linear
US-09-468-433C-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               281 EYVIKVSARVRFFFPS 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     281 EYVIKVSARVRFFFPS 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EYVIKVSARVRFFFPS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EYVIKVSARVRFFFPS 16
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Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
US-09-392-714-29
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US-08-465-167A-46
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Patent No. 6680191
GENERAL INFORMATION:
APPLICANT: LUCAS, Sophie; BOON-FALLEUR, Thierry
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES CODING FOR
TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PRECURSORS OF MEMBERS OF THE MAGE-C AN ITTLE OF INVENTION: MAGE-B FAMILIES AND USES THEREOF
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 309;
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                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage COMPUTER: LBM PS/2 COMPUTER: Diskette, 3.5 inch, 360 kb storage COMPUTER: LBM PS/2 COMPUTER: Diskette, 3.5 inch, 360 kb storage COMPUTER: LBM PS/2 COMPUTER: DISKET COMPUTER: DISKET COMPUTER: Wordperfect CURRENT APPLICATION NUMBER: US/09/066,281B FILING DATE: April 24, 1998 CLASSIFICATION NUMBER: US/09/066,281B FILING DATE: April 24, 1998 CLASSIFICATION NUMBER: 08/845,528 FILING DATE: April 25, 1997 ATTORNEY/AGENT INFORMATION: NAME: WATY Anne Schoffeld REGISTRATION NUMBER: 36,669 REGISTRATION NUMBER: 36,669 REGISTRATION NUMBER: 36,669 REGISTRATION NUMBER: 36,669 REGISTRATION NUMBER: 319.3100 TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 318-3100 TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 752-5958 INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/468,433C
FILING DATE: December 17, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 80; DB 4; 100.0%; Pred. No. 1.7e-06; tive 0; Mismatches 0;
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Fulbright & Jaworski L.L.P. STREET: 801 Pennsylvania Avenue, NW CITY: Washington STATE: District of Columbia COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acids
STRANDEDNESS: single stranded
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
PRILING DATE: April 24, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           281 EYVIKVSARVRFFFPS 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0
Matches 16; Conservative
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US-09-066-281B-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-468-433C-10
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57.5%; Score 46; DB 1; Length 10; 100.0%; Pred. No. 0.045; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 595, Application US/08159339A; Sequence 595, Application US/08159339A; Patent No. 6037135; GENERAL INFORMATION:
APPLICANT: Kubo, Ralph T.
APPLICANT: Sette, Alessandro
APPLICANT: Cells, Esteban
TITLE OF INVENTION: HIA Binding peptides and Their TITLE OF INVENTION: Uses
NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTRY: USA
ZIP: 94111-3834
COMPUTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSCE for Windows Version 2.0
SOFTWARE: 2000 SOS
FILING DATE: 07-AUG-1993
APPLICATION NUMBER: US 08/027,746
FILING DATE: 07-AUG-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
APTORNEY/AGENT INFORMATION:
NAME: Webber, Ellen Lauver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 018623-005030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                           ATTORNEY TABON THORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-60-1
TELECOMMUNICATION:
TELEPHONE: 206-467-9600
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 aming acids
       US 08/103,623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 57.5
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-465-167A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 YVIKVSARVR 10
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       APPLICATION NUMBER:
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Sequence 15, Application US/08465167A

Patent No. 5750395

GENERAL INFORMATION:
APPLICANT: Fikes, John D.
APPLICANT: Livingston, Brian D.
APPLICANT: Sette, Alessandro D.
APPLICANT: Sidney, John C.
TITLE OF INVENTION: IMMUNOGENIC PEPTIDES (as amended)
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Twomeend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61.3%; Score 49; DB 1; Length 10; 100.0%; Pred. No. 0.013; tive 0; Mismatches 0; Indels
                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,167A
FILING DATE: 05-JUN 1995
CLASSIFICATION: 435
PRIOR APPLICATION WHERE: US 08/103,623
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,167A
FILING DATE: OS-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14137-60-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 98111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 1413'
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 10 amino acids
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Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 KVSARVRFFF 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KVSARVRFFF 10
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                                                                                                                    USA
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US-08-465-167A-36
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                                                                                                                                                                                                                                                                                                                                                     Sequence 15, Application US/08627820
Patent No. 6464980
GENERAL INFORMATION:
APPLICANT: Fixes, John D.
Livingston, Brian D.
Sette, Alessandro D.
Sidney, John C.
TITLE OF INVENTION CLONING AND CHARACTERIZATION OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMIE: CA
COUNTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OMPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,820
FILING DATE: 02-APF-1996
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/103,623
APPLICATION DATA:
APPLICATION DATA:
ANDER SATEMATION:
NAME: PARMEDIE: CUNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: PARMEDIE: 21,990
REFERENCE/DOCKET NUMBER: 11,990
REFERENCE/DOCKET NUMBER: 11,390
TELECOMMINICATION INFORMATION:
MENT PRINTANTION INFORMATION:
TELECOMMINICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Street Tower CITY: San Francisco
                                                                                                                        57.5%; Score 46; DB 3; Length 10; 100.0%; Pred. No. 0.045; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4; Length 10; 0.045;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-08-627-820-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (206) 467-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 10 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.(
Matches 10; Conservative
                                                                                                                      Query Match
Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
NOLECULE TYPE: peptide
US-08-159-139A-595
                                                                                                                                                                                                           2 YVIKVSARVR 11
                                                                                                                                                                                                                                  1 YVIKVSARVR 10
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RESULT 14

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Gaps
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0
Sequence 36, Application US/08465167A
Sequence 36, Application US/08465167A
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Fikes, John D.
APPLICANT: Sette, Alessandro D.
APPLICANT: Sidney, John C.
TITLE OF INVENTION: IMMUNGENIC PEPTIDES (as amended)
TITLE OF INVENTION: IMMUNGENIC PEPTIDES (as amended)
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 44; DB 1; Length 9; Pred. No. 3e+05; 0; Mismatches 0; Indels
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US-08-465-167A-31
Sequence 31, Application US/08465167A
Sequence 31, Repair of the sequence 31, Application US/08465167A
Setent No. 575035
GENERAL INFORMATION:
APPLICANT: Fikes, John D.
APPLICANT: Sette, Alessandro D.
APPLICANT: Sidney, John C.
TITLE OF INVENTION: DNA ENCODING MAGE-1 C-TERMINAL
TITLE OF INVENTION: IMMUNOGENIC PEPTIDES (as amended)
                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,167A
FILING DATE: 05-JUN-1995
CLASSIFICATION 1995
PRIOR APPLICATION WHEER: US/08/103,623
FILING APPLICATION NUMBER: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: PATENTER 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: PATENTER 07-AUG-1993
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 11,990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEF. Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55.0%; Scc...
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VSARVRFFF 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||||||||||
1 VSARVRFFF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Lac 9; Conserv?
                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 98111
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ZIP: 98111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURSEITOATION NATA:
FILING DATE: 05-JUN-1995
CLASSIFICATION NUMBER: US 08/103,623
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Patenele, Steven W.
REGISTRATION NUMBER: 31,990
REPRENCE/DOCKET NUMBER: 14137-60-1
TELEPHONE: 206-467-9600
TELEPRATION NUMBER: 131,990
TELEPRATION NUMBER: 131,990
TELEPRATION NUMBER: 131,900
TELEPRATION NUMBER: 31,990
TELEPRATION NUMBER: 31,990
TELEPRATION NUMBER: 31,990
TELEPRATION STEATH OF SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: Amino Amino Amino Amino Amino Amino Amino Amino Amino A
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1 KVSARVRFF 9
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Search completed: October 7, 2004, 15:19:25 Job time : 17.4545 secs

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Scoring table:

Searched:

Minimum DB Maximum DB

Database

Perfect score:

Sequence:

OM protein

Run on:

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Sequence 57, Appl Sequence 2182, Appl Sequence 2182, Appl Sequence 13, Appl Sequence 13, Appl Sequence 113, Appl Sequence 4195, App Sequence 4195, App Sequence 111, Appl Sequence 111, Appl Sequence 27421, Sequence 274271, Sequence 5719, App Sequence 5719, App Sequence 3719, App Sequence 3714, App Sequence 3711, App Sequence 3711,
                        Sequence 5
Sequence 1
Sequence 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Thompson, Scott A
APPLICANT: Ramshaw, Ian A
TITLE OF INVENTION: Synthetic molecules and uses therefor
FILE REFERENCE: Savine
CURRENT APPLICATION NUMBER: US/10/296,734
CURRENT FILING DATE: 2003-08-04
PRIOR APPLICATION NUMBER: AU PQ7761/00
PRIOR FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 1507
SOFTWARE: Patentin version 3.2
SEQ ID NO 1278
2 US-10-218-095-2
4 US-10-1157-031-152
6 US-10-117-937-129
6 US-10-437-963-131272
6 US-10-753-158-56
2 US-10-753-158-56
2 US-10-128-711-93
4 US-10-128-711-93
4 US-10-128-711-93
4 US-10-128-711-93
5 US-10-128-711-93
6 US-10-128-711-152
7 US-10-149-138-4195
6 US-10-149-138-4195
6 US-10-149-138-4195
7 US-10-149-138-4195
8 US-10-149-138-4195
9 US-10-170-385-305
9 US-10-170-385-305
1 US-09-815-242-5719
0S-09-815-242-5719
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US-10-437-963-168711
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ilarity 100.0%; Pred. No. 6.8e-07;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 1278, Application US/10296734; Publication No. US20040054137A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: MAGE-1 segment 19
US-10-296-734-1278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 2, Application US/09766889A
; Patent No. US20020164654A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16
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                                                                                                                                                                                                                                                         592
1070
1070
679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
ses 16; Conserv
    10-296-734-1278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-766-889A-2
      LENGTH: 30
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Best Local S
Matches 16
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Sequence 18, Appl
Sequence 10, Appl
Sequence 71, Appl
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equence 2, Appli
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Sequence 828, App
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                                                                                                                               October 7, 2004, 15:30:52 ; Search time 59.6364 Seconds (without alignments) 86.336 Million cell updates/sec
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Sequence 32,
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Sequence 6,
Sequence 7,
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Sequence
Sequence
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/PCT_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW PUB.pep:*
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                                                                                                                                                                                                                                                                                                                                                                                             1351062
                    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-296-734-1278
US-09-766-889A-2
US-10-296-734-828
US-10-10-085-108-10
US-10-177-390-18
US-10-177-390-18
US-10-177-390-18
US-10-177-390-18
US-10-177-390-18
US-10-177-391-10
US-10-741-466-6
US-10-741-466-8
US-10-741-466-8
US-10-296-734-1280
US-10-296-734-1280
US-10-164-121A-33
                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                    1351062 segs, 321799191 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                 - protein search, using sw model
                                                                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                     1 EYVIKVSARVRFFFPS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                seq length: 0
seq length: 200000000
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Match Length DB
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80
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Gaps

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Score

8

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RESULT 5
US-10-177-390-18
is Sequence 18, Application US/1017390
is Bequence 18, Application WS/1017390
is Bequence 18, Application No. US20030143743A1
is GENERAL INFORMATION:
is APPLICANT: Schuler, Gerold
is APPLICANT: N.V. Antwerps Innovatiecentrum
is TITLE OF INVENTION: Polynucleotides by Electroporation
is TITLE OF INVENTION: Polynucleotides by Electroporation
is FILE REFERENCE: 021505wo/VH/ml
is CURRENT FILING DATE: 2002-06-20
is NUMBER OF SEQ ID NOS: 34
is SOFTWARE: PatentIn Ver. 2.1
is LENOTH: 309
it TYDE: PRT
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                                                                                                                                  ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Mary Anne Schofield
REGISTRATION NUMBER: 36,669
REFERENCE/DOCKET NUMBER: LUD 5611.1 JEL/MAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 80; DB 14;
100.0%; Pred. No. 7.8e-06;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
100.0%; Score 80; DB 13;
Best Local Similarity 100.0%; Pred. No. 7.8e-06;
Matches 16; Conservative 0; Mismatches 0;
           ADDRESSEE: Fulbright & Jaworski L.L.P. STREET: 666 Fifth Avenue CITY: New York City STATE: New York
                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/10/085,108
FILING DATE: 01-Mar-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 09/501,104
FILING DATE: 09-Feb-2000
APPLICATION NUMBER: 09/468,433
FILING DATE: December 17, 1999
APPLICATION NUMBER: 09/066,281
FILING DATE: APPLI 24, 1998
APPLICATION NUMBER: 08/845,528
FILING DATE: APFLI 25, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acids
STRANDEDNESS: single stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3100
                                                                                                                                                                                                      COMPUTER: IBM PS/2
OPRRATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (212) 318-3400 INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              281 EYVIKVSARVRFFFPS 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EYVIKVSARVRFFFPS 16
                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 16, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-10-177-390-18
                                                                                                                       COUNTRY:
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                                                          APPLICANT: Demotte, Nathalie
APPLICANT: Schultz, Erwin
TITLE OF INVENTION MAGE ANTICENIC PEPTIDES WHICH BIND HIA-B34 AND HIA-B44
FILE REPERENCE: L0461/7104
CURRENT APPLICATION NUMBER: US/09/766,889A
CURRENT FILING DATE: 2001-01-19
PRIOR PILING DATE: 2000-01-20
PRIOR APPLICATION NUMBER: US 60/177,242
PRIOR PILING DATE: 2000-01-26
NUMBER OF SEQ ID NOS: S9
SOFTHARE: RestSEQ for Windows Version 3.0
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Sequence 10, Application US/10085108

Publication No. US20020176865A1

GENERAL INFORMATION:

APPLICANT: LUCAS, Sophie; BOON-FALLEUR, Thierry

TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES CODING
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Publication No. US20040054137A1

GENERAL INFORMATION:

APPLICANT: Thompson, Scott A

APPLICANT: Thompson, Scott A

TITLE OF INVENTION: Synthetic molecules and uses therefor
FILE REFERENCE: Savine

CURRENT APPLICATION NUMBER: US/10/296,734

CURRENT FILING DATE: 2003-08-04

PRIOR FILING DATE: 2000-05-26

NUMBER OF SEQ ID NOS: 1507

SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 309;
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Pred. No. 7.8e-06;
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Best Local Similarity 100.0%; Pred. No. 7.8e-06;
Matches 16; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , OTHER INFORMATION: MAGE-1 consensus polypeptide US-10-296-734-828
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Boon-Falleur, Thierry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
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                                                 Stroobant, Vincent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial
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LENGTH: 309
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APPLICANT:
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Gaps
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TITLE OF INVENTION: Vaccine Compositions and Methods
FILE REPERENCE: 2595-003
CURRENT APPLICATION NUMBER: US/10/741,466
CURRENT FILING DATE: 2003-12-19
                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 80; DB 15; Best Local Similarity 100.0%; Pred. No. 7.8e-06; Matches 16; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 7.8e-06;
tive 0; Mismatches 0;
                 CURRENT APPLICATION NUMBER: US/10/117,937
CURRENT FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: US 60/282,211
PRIOR PILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: US 60/337,017
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 602
SEQ ID NO 71
LENGTH: 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Diamond, David C.
APPLICANT: Liu, Liping
APPLICANT: Liu, Liping
APPLICANT: Liu, Liping
TITLE OF INVENTION: EPITOPE SEQUENCES
FILE REFERENCE: MANIK. 032A
CURRENT APPLICATION NUMBER: US/10/657,022
CURRENT FLING DATE: 2003-09-04
PRIOR PLING DATE: 2002-09-06
PRIOR FLING DATE: 2002-09-06
NUMBER OF SEQ ID NOS: 610
SOFTWARE: FASTSEQ for Windows Version 4.0
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PRIOR APPLICATION NUMBER: 60/435,500
PRIOR FILING DATE: 2002-12-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 71, Application US/10657022; Publication No. US/20040180354A1; GENERAL INFORMATION: APPLICANT: Simmard, John J. L.; APPLICANT: Diamond, David C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/10741466; Publication No. US20040180058A1; GENERAL INFORMATION:
APPLICANT: Shreider, M.
APPLICANT: Shreider, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            281 EYVIKVSARVRFFFPS 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          281 EYVIKVSARVRFFFPS 296
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CTLIMM.027A
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Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
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US-10-657-022-71
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PRT
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US-10-741-466-6
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                                                                                                                                                                                                                                                APPLICANT: LUCAS, Sophie; DE SMET, Charles; BOON-FALLEUR, Thierry
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE CODING
FOR TUMOR REJECTION ANTIGEN PRECURSOR MAGE-C1 AND MAGE-C2
AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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WINDIUM TYPE: Diskette, 3.5 inch, 360 kb storage mobiled by 10.03

OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRITY APPLICATION WINBER: US/10/160,237

FILING DATE: 04-Jun-2002
CLASSIPTCATION: CURRICY
APPLICATION: CURRICY
RAPLICATION: CURRICY
APPLICATION: CURRICY
APPLICATION: WINBER: US/09/066,281B
FILING DATE: April 24, 1998
APPLICATION NUMBER: 08/09/066,281B
FILING DATE: April 24, 1998
APPLICATION NUMBER: 08/09/066,281B
FILING DATE: April 24, 1998
APPLICATION NUMBER: 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Mary Anne Schofield
REGISTRATION VINBER: 36,669
REFERENCE/DOCKET NUMBER: UID 5455.2 US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 20
CORRESSONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 10: US-10-160-237-10
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STRANDEDNESS: single stranded
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APPLICANT: SIMARD, John, J.L.
APPLICANT: DIAMOND, David, C.
APPLICANT: LIU, Liping
APPLICANT: XIE, Zhidong
TITLE OF INVENTION: EPITOPE SEQUENCES
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Publication No. US20030220239A1
GENERAL INFORMATION:
                                                                                                                                                                                Sequence 10, Application US/10160237
Publication No. US20030170256A1
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                              281 EYVIKVSARVRFFFPS 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         281 EYVIKVSARVRFFFPS 296
                   EYVIKVSARVRFFFPS 16
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Best Local Similarity 100.
Matches 16; Conservative
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US-10-296-734-1454
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                                                                                 Length 309;
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                                                                                                                        Indels
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Fublication No. US20040180058A1
GENERAL INFORMATION:
APPLICANT: Sherman, M.
APPLICANT: Sherman, M.
APPLICANT: Sherman, M.
TITLE OF INVENTION: Vaccine Compositions and Methods
FILE REFERENCE: 25955-003
CURRENT FILING DATE: 2003-12-19
FRIOR APPLICATION NUMBER: 60/415,500
FRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
IENGTH: 311
                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/10741466
Publication No. US20040180058A1
GENERAL INFORMATION:
APPLICANT: Sherman, M.
TITLE OF INVENTION: Vaccine Compositions and Methods
FILE REPERENCE: 25955-003
CURRENT APPLICATION NUMBER: US/10/741,466
CURRENT FILING DATE: 2003-12-19
PRIOR APPLICATION NUMBER: 60/435,500
PRIOR APPLICATION NUMBER: 60/435,500
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIN Ver. 2.1
                                                                                 Query Match
100.0%; Score 80; DB 16;
Best Local Similarity 100.0%; Pred. No. 7.8e-06;
Matches 16; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 7.9e-06; Matches 16; Conservative 0; Mismatches 0;
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; TYPE: PRT
; ORGANISM: Influenza A virus
US-10-741-466-6
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; ORGANISM: Influenza A virus
US-10-741-466-7
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; ORGANISM: Influenza A virus
US-10-741-466-8
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Matches
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Sequence 1280, Application US/10296734

Publication No. US20040054137A1

GENERAL INFORMATION:
APPLICANT: Ramshaw, Ian A

TITLE OF INVENTION: Synthetic molecules and uses therefor FILE REFERENCE: Source
CURRENT FILING DATE: 2003-08-04

PRIOR APPLICATION NUMBER: US/10/296,734

CURRENT FILING DATE: 2000-05-26

NUMBER OF SEQ ID NOS: 1507

SOUTWARE: PatentIn version 3.2

LENGTH: 28
                                                                APPLICANT: Thompson, Scott A

APPLICANT: Ramshaw, Ian A

TITLE OF INVENTION: Synthetic molecules and uses therefor
FILE REFERENCE: Savine
CURRENT APPLICATION NUMBER: US/10/296,734

CURRENT PILING DATE: 2003-08-04

PRIOR APPLICATION NUMBER: AU PQ7761/00

PROR FILING DATE: 2000-05-26

NUMBER OF SEQ ID NOS: 1507

SOFTWARE: Patentin version 3.2

SEQ ID NO 1454

LENGTH: 3541
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100.0%; Pred. No. 0.00042;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 80; DB 12;
100.0%; Pred. No. 0.0001;
tive 0; Mismatches 0;
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; OTHER INFORMATION: MAGE-1 segment 20
US-10-296-734-1280
Sequence 1454, Application US/10296734 Publication No. US20040054137A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 33, Application US/10164121A
Publication No. US20030228308A1
GENERAL INFORMATION:
APPLICANT: Zhang, Yi
APPLICANT: Boon, Thierry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1704 EYVIKVSARVRFFFPS 1719
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Best Local Similarity 100...
The conservative conservative
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Best Local Similarity 100.
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Artificial
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ORGANISM: Artificial
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Publication No. US20030228325A1

Publication No. US20030228325A1

GENERAL INFORMATION:

APPLICANT: Bilaborough, Janine
APPLICANT: Bilaborough, Janine
APPLICANT: Barugaen, Pierre
APPLICANT: Panichelli, Christophe
APPLICANT: Van der Buruggen, Pierre
APPLICANT: Van der Pierre
APPLIC
APPLICANT: Van der Bruggen, Pierre
APPLICANT: Traversari, Catra
TITLE OF INVENTION: 150-1ated Peptides Which Bind to HLA-Cw6 Molecules And Uses Thereq
FILE REFERENCE: LUD-5-71
CURRENT APPLICATION NUMBER: US/10/164,121A
CURRENT FILING DATE: 2002-08-26
NUMBER OF SEQ ID NOS: 36
SEQ ID NO 33
LENGTH: 12
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; ORGANISM: H. sapiens
; FEATURE:
US-10-164-121A-33
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ORGANISM: H. sapiens
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GenCore version 5.1.6

Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 7, 2004, 15:17:11; Search time 18.5455 Seconds
(without alignments)
82.989 Million cell updates/sec
Title: US-09-336-091-4
Perfect score: 80
Sequence: 1 EYVIKVSARVRFFFPS 16
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366
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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Listing first 45 summaries

1: pir:\*
2: pir2:\*
3: pir2:\*
4: pir4:\*

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	scrip	melanoma antiden M	₩.	unknown protein, 4	hypothetical prote		NH(3	probable bis(5'-nu	6-phospho-beta-glu	hypothetical prote	14		hypothetical prote	>	hypothetical prote		ribosomal large ch	hypothetical prote	oxidoreductases ho	oxidoreductases ho	hypothetical prote		hypothetical prote	alpha-glucosidase	protein T4012.19 (	hypothetical prote	ribosomal protein	ribosomal protein		ABC-type transport
SUMMARIES	ΙD	138661	A54600	H86416	F98257	AD3027	E71282	H82322	E89790	872753	H81427	S41790	T22909	S61703	T26774	H70459	AI1195	D96769	AI1691	AI1319	H71122	T33155	S57974	H97033	D96788	T33188	JC4911	A42735	JC2013	T00107
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protein F28J9.7 [i	hypothetical prote	acetyl-CoA carboxy	thioredoxin reduct	hypothetical prote	hypothetical prote	hypothetical prote	conserved hypothet	asparty1-tRNA synt	aspartate-tRNA lig	hypothetical prote	hypothetical prote	L-JAK protein-tyro	protein stn-B - fr	probable polyketid	hypothetical prote
B86486	T26383	AF3504	G69759	T21450	E69294	A70434	F72265	G81195	F81831	T02734	T40994	A55747	T13353	T17420	G81737
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270	288	301	336	428	468	477	594	602	602	720	821	1124	1262	2458	122
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36	36	36	36	36	36	36	36	36	36	36	36	36	36	36	35.5
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. 4.	45	35.5	4.4	•	122	.0	G81737					hyp	hypothetical	ical	prote	5 W	
							ALI	ALIGNMENTS	TS								
RESULT 13861 melano N;Alte	RESULT 1 138661 melanoma antigen MAGE-4 N'Alternate names: MAGE C'Species: Homo ganione	ntige: e name	n MAG	E-4 .	- human 41 prot	n tein	; mel	- human 41 protein; melanoma antigen MAGE-X2 (man)	anti	gen	AAGE-	23					
C; Dat C; Dat C; Acc R; De	C.Date: 07-Jun-1996 #sequence revision 07-Jun-1996 #text change 18- C.Accession: 138661; 138662; PH1297; PH1298; JC2359; G01446 R.De Plaen, E.; Arden, K.; Traversari, C.; Gaforio, J.J.; Szikora,	-Jun- n: 13	1996 1996 8661; Ardel	#segu I386 n, K.	ence 62; P	revi H129 Vers	sion 7; PH ari,	07-Ju 11298; C.; G	n-199 JC23 afori	6 #te 159; C	30144 3017	hange 6 Sziko		change 18-Feb-2000 46 Szikora, J.P.; De		Smet,	ς:
Immun A;Tit	DOUN, 11.00 and 40, 360-369, 1994 A/Title: Structure, chromosomal localization, and expression of A/Reference number: 138659; MUID:95012457; PMID:7927540	tics tructi e numi	40, 3 ure, ber:	60-36 chrom I3865	9, 19 osoma 9; MU	94 1 10 1D:9	caliz 50124	ation 157; F	, and	l exp	ressi 10	o uo		genes	of	the 1	MAGE
A; Res A; Res A; Res A; Res A; Cro	A;ACCEBSION: 138001 A;Status: prellminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-317 <dep1> A;Cross-references: EMBL:U10687; NID:g533514; PIDN:AAA68871.1;</dep1>	prelin type : 1-3:	minar : DNA 17 <di< td=""><td>y; tr EP1&gt; EMBL:</td><td>ansla U1068</td><td>ted 7; N</td><td>Erom ID:95</td><td>GB/EN</td><td>BL/DE</td><td>IBJ IN: AAJ</td><td>16887</td><td>1.1;</td><td>PID:</td><td>PID:953351</td><td>115</td><td></td><td></td></di<>	y; tr EP1> EMBL:	ansla U1068	ted 7; N	Erom ID:95	GB/EN	BL/DE	IBJ IN: AAJ	16887	1.1;	PID:	PID:953351	115		
A; EXD A; Sta A; Mol	A,Experimental Bour A,Accession: 138662 A,Etatus: prelimina. A,Molecule type: DN. A,Residues: 1-172,"	ncal n: I3 prelit type type	Bource 8662 minar DNA:	e: an y; tr ',174	tigen ansla -317	mAG cDEP	2-4a From 2>	GB/EN	BL/DE	ВЈ				,			
A;Cro A;EXP R;Tra U. EXP	ss-re erime versa p. Me	ntal ri, C d. 17	source ., val 5, 14	EMBL: e: an n der 53-14	tigen Brug 57, 1	MAG MAG gen, 992	3-4b R.,	Luesc	, Pil	I F.	Lur	۲۰۱۶ عالمه	P. D.	chom Chom	lez,	 	Van Pel
A;Title: A nonapeptide encoded by human gene MAGE-1 is recognized on HLA-Al by: A;Reference number: PH1294; MUID:93018875; PMID:1402688 A;Accession: PH1297 A;Molecule type: DNA A;Residues: 169-177 <tra1></tra1>	le: A ession ecule	nonaj e numi n: PH: type : 169	peptionser: 1297	de en PH129 <tra1< td=""><td>coded 4; MU</td><td>Dy 10:9:</td><td>30188</td><td>1 gene</td><td>MID:1</td><td>-1 ie 4026</td><td>8 rec</td><td>ogni z</td><td>o p</td><td>recognized on HLA-Al by cytolytiv</td><td> A1</td><td>ίο<sub>.</sub> <b>λ</b>α</td><td>,tol)</td></tra1<>	coded 4; MU	Dy 10:9:	30188	1 gene	MID:1	-1 ie 4026	8 rec	ogni z	o p	recognized on HLA-Al by cytolytiv	A1	ίο <sub>.</sub> <b>λ</b> α	,tol)
A; EXP A; ACC A; MOL A; Res A; Esp	erime ession ecule idues	ntal n: PH: type : 169	Source 1298 : DNA -172, Source	e: an 'T',1 e: an	tigen 74-17 tigen	MAGI MAGI	3-4 3-41		,								
R; Din Bioch A; Tit A; Ref	lg, M. lem. B. lerenci erenci	iophy iophy loning e num n: JC	s. Rei g and oer:	J., K B. Col anal JC235	eller mmun. ysis 8; MU	, C.v.	J.; F 549 AGE-1	enton -555, -rela 35; P	, R.G 1994 ted 9 MID:8	enes 03776	. 13						
A; Molecule type: mkNA A; Residues: 1-172, '17, 174-306,'Q', 308-317 <din> A; Residues: 1-172, '17, 174-306,'Q', 308-317 <din> A; Residues: EMBL:U10340; NID:g499123; PIDN:AAA19007.1; PID:g499124 A; Experimental source: melanoma cell line DM150 C; Genetics: GDB:MAGE4; MAGE4; MAGE-X2 A; Gene: GDB:MAGE4; MAGE-X2 A; Cross-references: GDB:331119 A; Map position: Xq28-Xq28</din></din>	A;Nolecule Uype: mxvA A;Residues: 1-172,' x74-306, A;Cross-references: EMBL:U1034 A;Experimental source: melanom C;Genetics: A;Gene: GDB:MAGEA4, MAGE4; MAG A;Cross-references: GDB:331119 A;Map position: Xq28-Xq28	coule type: mxna dues: 1712, 'T' 174 is-references: BMBL: xrimental source: me trics: :: GDB:MAGEA4; MAGE4 :: cferences: GDB:3 position: Xq28-Xq28	: mkN 72, T 72, T 50urce 50urce 54, T 768: (	A, 174 EMBL: E: me MAGE4 GDB:3:	-306, U1034 lanom ; MAG	0', 0', N', E-X2	308-3 ID:94 Il li	17 < D	IN> ; PID 150	N: AA	11900	7.1;	PID:	94991	24		•
A; Int C; Sup F; 169	A;Introns: #status absent C;Superfamily: tumor associated protein MAGE F;169-177/Region: HLA-Al binding #status predicted	#sta! ily: ( Regio	tus al tumor 1: HL	bsent asso A-A1	ciate bindi	d pro	otein statu	MAGE	dicte	Ţ							

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hypothetical protein AGR_L_2017 [imported] - Agrobacterium tumefaciens (strain C58, Cer C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Species: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
C;Accession: F98257
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B., Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein Atu3824 [imported] - Agrobacterium tumefaciens (strain C58, Dupont) C5Species: Agrobacterium tumefaciens C5Decies: Agrobacterium tumefaciens C5Decies: Agrobacterium tumefaciens C5Decies: Agrobacterium tumefaciens C5Decies: Agrobacterium tumefaciens C5Bccssion: AD3027
R5Mcod, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I R5Mcod, D.W.; Setubal, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E71282
probable NH(3)-dependent NAD(+) synthetase (nadE) - syphilis spirochete
C;Species Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999
C;Accession: E71282
C;Accession: E71282
Frasser, C.M.; Norxis, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwirrson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDcthey, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Reference number: AB2577; MUID:21608550; PMID:11743193
A,Accession: AD3027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: GB: AE007870; PIDN: AAK89584.1; PID: g15159473; GSPDB: GN00170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Molecule type: DNA
A,Restidues: 1-327 <KNR>
A,Cross-references: GB:AE008689, PIDN:AAL44634.1; PID:g17742257; GSPDB:GN00187
A,Experimental source: strain CS8 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Pred. No. 10;
3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 40; DB 2;
Pred. No. 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Map position: linear chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 46.7%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  207 QYFKKMGLRVRYFMP 221
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Best Local Similarity 46.7%;
Matches 7; Conservative
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A Molecule type: DNA
A, Residues: 1-327 < KUR>
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A, Gene: AGR_L_2017
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C; precises Homo sapiens (man)
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C; Accession: A54600
R; Hu, P.; Mondino, A.; Skolnik, E.Y.; Schlessinger, J.
Mol. Call. Biol. 13, 7677-7688, 1993
A; Title: Cloning of a novel, ubiquitously expressed human phosphatidylinositol 3-kinase
A; Reference number: A54600; MUID:94067128; PMID:8246984
A; Accession: A54600
A; Residues: 1-1070 cHUI>
A; Residues: 1-1070 cHUI>
A; Residues: 1-1070 cHUI>
A; Residues: 1-1070 cHUI>
A; Cossereferences: GB:567334; NID:9455759; PIDN:AAB29081.1; PID:9455760
A; Note: sequence extracted from NCBI backbone (NCBIN:140879; NCBIP:140880)
C; Genetics: A; Cross-references: GB:136233
C; Superfamily: phosphatidylinositol 3-kinase
C; Keywords: phosphotransferase
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RiTheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

Ajauthors: Hunger, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Ajauthors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Title: Sequence and analyais of chromosome 1 of the plant Arabidopsis.
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A;Molecule type: DNA
A;Residues: 1-132 <STO>
A;Cross-references: GB:AE005172; NID:g10092214; PIDN:AAG12630.1; GSPDB:GN00141
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                             phosphatidylinositol 3-kinase (EC 2.7.1.137) 110K chain beta isoform - human
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                 Length 317;
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                                                                                            2; Indels
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                              Score 51; DB 2;
Pred. No. 0.076;
                                                                                            Mismatches
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50.0%; Pred. No. 4;
ive 3; Mismatches
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د
                                                                                                                                                                                   289 EHVVRVNARVRIAYPS 304
                              63.7%;
56.2%;
                                                                                                                                                       1 EYVIKVSARVRFFFPS 16
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                                                                                            Conservative
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Query Match
Best Local Similarity
The 9; Conserve
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Best Local Similarity
7, Conserve
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Matches 7; Conserv
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A;Cross-references: EMBL:299125; NID:g2398683; PIDN:CAB16170.1; PID:e343547; PID:g23987:
C;Genetics:
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B; Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillis C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barre C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barre A; G. 665-668, 2000

A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hy A;Reference number: A81250; MUID:20150912; PMID:10688204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AL139074; GB:AL111168; NID:g6967505; PIDN:CAB72596.1; PID:g69676
A;Experimental source: serotype O2, strain NCTC 11168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           periplasmic protein Cj0112 [imported] - Campylobacter jejuni (strain NCTC 11168)
C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cispecies: Mycobacterium leprae
Cibate: 19-War-1997 #sequence_revision 25-Apr-1997 #text_change 23-Mar-2001
Cibate: 19-War-1997 #sequence_revision 25-Apr-1997 #text_change 23-Mar-2001
Cibate: 19-War-1997 #sequence_revision 25-Apr-1997 #text_change 23-Mar-2001
Cibate: 19-War-1997 #sequence_revision 23-Mar-2001
Rismith D.R.; Robison, K.
Submitted to the EMBL Data Library, November 1993
A; Description: Mycobacterium leprae cosmid B1496.
A; Rescrence number: 372695
A; Moccasion: 872753
A; Mo
                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein B1496_C1_154 - Mycobacterium leprae
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-392 <PAR>
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Pred. No. 30;
3; Mismatches
                                                                                                      DB
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Pred. No. 29;
                                                                                                                                          Pred. No. 23;
4; Mismatches
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A;Gene: bglA
C;Superfamily: Agrobacterium beta-glucosidase
                                                                                                      Score 39;
Pred. No.
                                                                                              veery march
Best Local Similarity 54.5%;
Matches 6; Conservative
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53.8%;
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208 VVRVSANVRFSGP 220
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Best Local Similarity 61.57
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Best Local Similarity 53.0.
7; Conservative
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257 QIANRLRFFFP 267
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A,Molecule type: DNA
A,Residues: 1-402 <PAR>
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A;Experimental source: strain Nichols
C;Genetics:
A;Gene: TP0780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-269 <HEI>
A;Cross-references: GB:AE004131; GB:AE003852; NID:g9654856; PIDN:AAF93614.1; GSPDB:GN001
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
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C;Superfamily: bis(5'-nucleosyl)-tetraphosphatase (symmetrical); phosphoesterase core hc
C;Keywords: hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable bis(5'-nucleosy1)-tetraphosphatase (symmetrical) (EC 3.6.1.41) VC0441 [similari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: H82322
S;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vemathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, E.
I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Atture 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
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C;Dates: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: E89790
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.;
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu,
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
          A; Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete. A; Reference number: A71250; MUID: 98332770; PMID: 9665876
A; Accession: B71282
A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA
A; Residues: 1-679 <COL>
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A;Residues: 1-478 «KUR»
A;Cross_references: GB:BA000018; PID:g13700182; PIDN:BAB41480.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUID:21311952; PMID:11418146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 31-Dec-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6-phospho-beta-glucosidase [imported] - Staphylococcus aureus (strain N315)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                        Length 679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 Score 40; DB 2;
Pred. No. 21;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 39; DB 2;
Pred. No. 13;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                 50.0%;
53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 42.9%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    173 YIVNAFTRMRFCFP 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : : | | | : | | 649 VNLSPRVGFYFPS 661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 IKVSARVRFFFPS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
Science 281, 375-388, 1998
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: E89790
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary A;Molecule type: DNA
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A; Accession: 502-505
A; Residues: 1-1887 < URBA>
A; Rieger, M.; Mueller-Auer, S.; Schaefer, M.
R; Rieger, M.; Mueller-Auer, S.; Schaefer, M.
R; Reference number: 565202
A; Reference number: 565202
A; Reference number: 565202
A; Reference number: 565202
A; Residues: 1567-1887 < RIE>
A; Residues: 1567-1887 < RIE>
A; Residues: 1567-1887 < RIE>
A; Cross-references: EMBL: 273587; MIPS: YPL231W
A; Residues: 1567-1887 < RIE>
A; Cross-references: EMBL: 273587; MIPS: YPL231W
A; Residues: 263, 12315-12325, 1988
A; Title: Primary structure of the multifunctional alpha subunit protein of yeast fatty a A; Reference number: A31107; MUID:88315020; PMID:2900835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-310,'TTGTGG',311-593,'I',595-940,'CLNCVKSWLKLLKLERQFPSKLLW','SIRLSMAIALMLH
A;Cross-references: EMBL:J03936; NID:g171501; PIDN:AAA34601.1; PID:g171502
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A;Introns: 69/3; 117/2; 186/3; 226/3; 268/3; 371/3; 540/3; 857/1; 881/3; 1025/3; 1077/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein ad 1854 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: O8-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C;Accession: H70459
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-1801 <WIL>
A;Cross-references: EMBL:AL032634; PIDN:CAB54418.1; GSPDB:GN00019; CESP:Y39G8C.b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ä
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C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 38; DB 2; Length 100. Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46.9%; Score 37.5; DB 2; 75.0%; Pred. No. 1.7e+02; ive 2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R.Smye, R. submitted to the EMBL Data Library, October 1998 A.Reference number: 220263 A.Accession: T26774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: SGD:S0006152; MIPS:YPL231w
A;Map position: 16L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Superfamily: yeast fatty-acid synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Keywords: acyltransferase; coenzyme A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1672 EYVAKVSAREKSAYKFF 1688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: clone Y39G8C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EYVIKVSAR----VRFF 13
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58.8%;
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Best Local Similarity 75.00,
Best Local 9, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity 58.8
Matches 10; Conservative
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840 VLKVSSR-RFFF 850
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A; Accession: S65256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
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                                                                                                        hypothetical protein 6 - thermophilic bacterium RTB.B4 (fragment)

C.Species: thermophilic bacterium RTB.B4

C.Species: thermophilic bacterium RTB.B4

C.Species: 07-Sep-1994 #sequence_revision 14-Feb-1997 #text_change 05-Nov-1999

C.Accession: $41790

R.Dwivedi, P.P.; Gibbs, M.D.; Bergquist, P.L.

R.Dwivedi, P.P.; Gibbs, M.D.; Bergquist, P.L.

R.Dwivedi, P.P.; Gibbs, M.D.; Bergquist, P.L.

A.Reference to the BMBL Bata Library, October 1993

A.Reference number: $41785

A.Recession: $41780

A.Recession: $41790

A.Rocession: $41790

A.Rocession: $41790

A.Rocession: $4170

A.Rocession: $4170

A.Rocession: $4170

A.Rocession: $4170

A.Rocession: $4170

A.Cossa-references: EMBL:L18965; NID:g311185; PIDN:AAB42046.1; PID:g552047
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N.Alternate names: protein P1409; protein YPL231w
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C;Species: Gaenorhabditis elegans
C;Species: Gaenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: T22909
R;Sims, M.; Lloyd, C.
R;Status: preliminary; Lranslated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rocession: T2290
A;Rolecule type: DNA
A;Residues: 1-610 <WIL>
A;Residues: 1-610 <WIL>
A;Coss.references: EMBL:Z81093; PIDN:CAB03147.1; GSPDB:GN00022; CESP:F58D2.2
A;Experimental source: clone F58D2
C;Genecics:
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C.Species: Saccharomyces cerevisiae
C.Date: 09-Mar-1996 #sequence revisiae
C.Date: 09-Mar-1996 #sequence revision
C.Accession: 861703; 865256; 865250; A31107
R.Urrestarazu, L.A.
R.Urrestarazu, L.A.
R.Data Library, December 1995
A.Reference number: 861699
A.Residues: 1.88703
A.Residues: 1.1887 vURR>
A.Residues: 1.1887 vURS>
A.Reference number: 865251
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A;Introns: 28/1; 93/1; 184/3; 242/3; 422/3; 540/2
C,Superfamily: Caenorhabditis elegans hypothetical protein T08B6.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47.5%; Score 38; DB 2; Length 610; 46.7%; Pred. No. 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 402
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Best Local Similarity 31.2%; Pred. No. 30;
Matches 5; Conservative 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361 ELVVKITKKINDYYPS 376
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Best Local Similarity 46.77
Conservative
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Nature 392, 353-358, 1998

A; Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A; Reference number: A70300; MuID:98196666; PMID:9537320
A; Reference number: A70300; MuID:98196666; PMID:9537320
A; Rocession: H70459
A; Residues: Dreliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA
A; Residues: 1-152 <AQP>
A; Cross-references: GB:AE000759; NID:g2984125; PIDN:AAC07670.1; PID:g2984134; GB:AE00065
A; Experimental source: strain VFS
C; Generics:
A; Gene: aq_1854
Query Match
Best Local Similarity 63.6%; Pred. No. 17;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Cy
S; KVSARVRFFPP 15
:|||||:|||
Db 68 EVSARVKFYP 78
Search completed: October 7, 2004, 15:18:17
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Kerry G., Greystrong J.S., Clark D., Goerdes M., Blechschmidt K., Rump A., Hinzmann B., Mundy C.R., Miller W., Poustka A., Herman G.E., Rhodes M., Denny P., Rosenthal A., Brown S.D.M.; "Comparative genome sequence analysis of the Bpa/Str region in mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUB-Blood:
MEDLINE-94157413; PubMed-8113684;
MEDLINE-94157413; PubMed-8113684;
Gaugler B., van den Bynde B., van der Bruggen P., Romero P.,
Gaforio J.J., de Plaen E., Lethe B., Brasseur F., Boon T.;
"Human gene MAGE-3 codes for an antigen recognized on a melanoma by autologous cytolytic T lymphocytes.";
J. Exp. Med. 179:921-930(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND VARIANT ALA-32.
Chen H., Wang L., Mei M., Qin L., Cong X., Xu J., Wei L.,
Chen W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The polymorphism of MAGE-1 gene in Chinese people.";
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and man.";
Genome Res. 10:758-775(2000)
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homo sapien
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bos taurus
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                                                                                                  7, 2004, 15:13:16; Search time 10.9091 Seconds (without alignments) 76.370 Million cell updates/sec
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Q8tc29
Q9pli5
Q67492
Q08200
P59065
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P43358
P43358
P935405
P95405
P95406
P9540
P95406
P9
5.1.6
Compugen Ltd.
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                                                                                                                                                                                                                                                                                                          141681 segs, 52070155 residues
GenCore version (c) 1993 - 2004
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NADE_TREPA
APAH_VIBCH
RPOC_OENOE
YE62_MYCLE
TOLB_CAMJE
YOR6_CALSR
FAS2_YEAST
YIS4_AQUAE
EKI1_YEAST
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RL10 BOVIN
RL10 HUMAN
RL10 MOUSE
Y163 BUCBP
YF45 AQUAE
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MAG4_HUMAN
P11B_HUMAN
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A11A MOUSE
STNB DROME
PKHD HUMAN
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YF34 AQUAE
RL10 CHICK
FPG SYNEL
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Maximum Match 100%
Listing first 45 summaries
                                                                     - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match Length DB
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Perfect score:
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Maximum DB E
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No.
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Wang

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Genew; HGNC:6802; MAGEA4.
                                                                                                                                                                                                                                                                                    rejection antigens.";
Gene 160:287-290(1995).
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                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                   SEQUENCE FROM N.A.
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      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation he Burbean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                             Schultz-Thater E., Juretic A., Dellabona P., Luscher U., Siegrist W., Harder F., Heberer M., Zuber M., Spagnoli G.C.;
"MAGE-I gene product is a cytoplasmic protein.";
Int. J. Cancer 59:435-439(1994).
Int. J. Subcrition Not known, though may play a role in embryonal development and tumor transformation or aspects of tumor progression. Antigen recognized on a melanoma by autologous cytolytic T lymphocytes.
INTSUE SPECIFICITY: Expressed in many tumors of several types, such as melanoma, head and neck squamous cell carcinoma, lung carcinoma and breast carcinoma, but not in normal tissues except
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10-OCT-2003 (Rel. 42, Last annotation update)
Melanoma-associated antigen 4 (MAGE-4 antigen) (MAGE-X2) (MAGE-41).
MAGEA4 OR MAGE4.
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TSSUR=BHOOd;
MEDLINE=95012457; PubMed=7927540;
de Plaen E., Arden K., Traversari C., Gaforio J.J., Szikora J.-P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                               for testes. Never expressed in kidney tumors, leukemias and
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FTId=VAR 004283.

FTId=VAR 011737.

/FTId=VAR 011737.

/FTId=VAR 011737.

Y->A: ABOLISHES HIA-A: BINDING.

Y->A: ABOLISHES HIA-A: BINDING.

W; 544EBBIF9F4E9D33 CRC64;
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DOMAIN 102 301 MAGE.
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Pred. No. 8.7e-08;
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                                                                                                                                                                                                                                                                 SIMILARITY: Contains 1 MAGE domain.
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InterPro: IRN002190; MAGE.
Pfam; PF01454; MAGE; 1.
PROSITE; PSS0838; MAGE; 1.
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EMBL, AX148466; AAN62752.1; -.
Genew, HGNC: 6796; MAGEA1.
MIM; 300016; -.
SUBCELLULAR LOCATION.
MEDLINE=95012905; PubMed=7927954;
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01-NOV-1995 (Rel. 32, Last seq
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169 1
309 AA;
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Best Local Similarity
Matches 16; Conserv
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P43358;
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SEQUENCE
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VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A MEDLINE=20380257; PubMed=12477932; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Rausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., A.A. Lechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., A. A. Lechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., A. A. Lecherko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., A. Brownstein M.J., Wickernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Anchards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Anhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Abraesley R.W., Touchman J.W., Green E.D., Dickson M.C., Abnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

Butterfield Y.S.N., Krzywinski M.I., Skalalaka U., Smailus D.E., Generation and initial analysis of more than 15,000 full-length Numan and mouse CDNA sequences ";

Proc. Natl. Acad. Sci. U.S.A., 99:16899-16903(2002).

C. PEUNCTION: NOT KNOWN, THOUGH MAY PLAY A ROLE IN EMBRYONAL DECENCE TO TUMOR DEVELOMENT AND TUMOR TRANSFORMATION OR ASPECTS OF TUMOR DEVELORERY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interpro; IPR002190; MAGE.
Pfam; PP01454; MAGE; 1.
PROSITE; PS5038; MAGE; 1.
Antigen; Multigene family; Polymorphism; Tumor antigen; 3D-structure.
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                                                                                                     of
de Smet C., Brasseur F., van der Bruggen P., Lethe B., Lurquin C., Brasseur K., Chomez P., de Backer O., Cavenee W., Boon T.; "Structure, chromosomal localization, and expression of 12 genes o the MAGE family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-95369706; PubMed=7642112;
Imai Y., Shichijo S., Yamada A., Katayama T., Yano H., Itoh K.;
"Sequence analysis of the MAGE gene family encoding human tumor-
                                                                                                                                                                                                                                                                                                                                                            TISSUE=Skin,
MEDLINE=94311915, PubMed=8037761;
Ding M., Beck R.J., Keller C.J., Fenton R.G.;
"Cloning and analysis of MAGE-1-related genes.";
Biochem. Biophys. Res. Commun. 202:549-555(1994).
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EMBL, U10688; AAA68872.1; -.
EMBL, U10340; AAA1907.1; -.
EMBL, D32077; BAA06843.1; -.
PMRJ, BC017723; AAH17723.1; -.
PIR; I38661; I38661.
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1070 AA;
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Q9Z1LO;
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01-NOV-1995 (Rel. 32, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-21004 (Rel. 43, Last annotation update)
19-Mosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit, beta isoform (RC.2.7.1.153) (Pl3-kinase pl10 subunit beta) (Ptdins-3-kinase pl10) (Pl3K) (Pl3Kbeta).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

Kossila M., Sinkovic M., Karkkainen P., Laukkanen M.O., Miettinen R.,
Kossila M., Sinkovic M., Kusisto J., Yla-Herttuala S., Laakso M.;
Rissanen J., Kekalainen P., Kuusisto J., Yla-Herttuala S., Laakso M.;
"Gene encoding the catalytic subunit pilobeta of human
phosphatidylinositol 3-kinase: cloning, genomic structure and
screening for variants in patients with type 2 diabetes.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
--- FUNCTION: PHOSPHORYLATES PTDINS, PTDINS4P AND PTDINS(4,5)P2
--- FUNCTION: PROSPHORYLATES PTDINS, PTDINS4P AND PTDINS(4,5)P2
--- PUNCTION: ATMINITY: ATP + 1-phosphatidyl-1D-myo-inositol 4,5-
bisphosphate = ADP + 1-phosphatidyl-1D-myo-inositol 3,4,5-
                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- PATHWAY: Signaling pathways regulating cell growth.
-i- SUBUNIT: HETERODIMER OF A P110 (CATALYTIC) AND A P85 (REGULATORY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=94067128; PubMed=8246984; Hu P., Mondino A., Skolnik E.Y., Schlessinger J.; Hu P., Mondino A., Skolnik E.Y., Schlessinger J.; "Cloning of a novel, ubiquitously expressed human phosphatidylinositol 3-kinase and identification of its binding site
                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                              ö
                                                                                             63.7%; Score 51; DB 1; Length 317;
larity 56.2%; Pred. No. 0.035;
Conservative 5; Mismatches 2; Indela
                            173 173 T -> A.

/FTId=VAR 004284.

307 307 E -> Q (IN REF. 2).

317 AA; 34929 MW; 3CFAC0E2B696257C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- TISSUE SPECIFICITY: Expressed ubiquitously.
-!- SIMILARITY: Belongs to the PI3/PI4-kinase family.
                                                                                                                                                                                                                                                            PRT; 1070 AA
MAGE.
POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cell. Biol. 13:7677-7688(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AJ297549; CAC21449.1; -.
EMBL; AJ297550; CAC21449.1; JOINED.
EMBL; AJ297551; CAC21449.1; JOINED.
EMBL; AJ297552; CAC21449.1; JOINED.
EMBL; AJ297553; CAC21449.1; JOINED.
EMBL; AJ297554; CAC21449.1; JOINED.
                                                                                                                                                                     |:|:||||| :||
289 EHVVRVNARVRIAYPS 304
                                                                                                                                                        1 EYVIKVSARVRFFFPS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; S67334; AAB29081.1; -.
                                                                                                                                                                                                                                                          STANDARD;
                                                                                                           Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
              41
173
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                                                                                                                                                                                                                                                          P11B HUMAN
              DOMAIN
                                                     CONFLICT
                                                                    SEQUENCE
                                                                                                Query Match
                                                                                                                                                                                                                                                                         P42338;
                                                                                                                                                                                                                                                                                                                                                                            PIK3CB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  on p85.
Mol. Ce
DOMAIN
                                                                                                                                                                                                                                          PIIB HUMAN
                                                                                                                                                                                                                               RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit, beta isoform (EC 2.7.1.153) (Pl3-kinase pl10 subunit beta) (Ptdins-3-kinase pl10) (Pl3K) (Pl3Kbeta).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mulder H., Stenson Holst L., Degerman B.; "Phosphatidylinositol-3 kinase and activation of phosphodiesterase 3B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Pred. No. 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IRR008938; ARM.
InterPro; IPR008938; ARM.
InterPro; IPR008938; ARM.
InterPro; IPR008939; C2 Calb.
InterPro; IPR009403; P13 P14 kinase.
InterPro; IPR003413; P13K_P85B.
InterPro; IPR003113; P13K_P85B.
InterPro; IPR001263; P13K_B85B.
InterPro; IPR001263; P13K_G2; 1.
Pfam; PF00792; P13K_C2; 1.
Pfam; PF00794; P13K_D2; 1.
Pfam; PF00796; P13K_D2; 1.
PF0STIE; P500915; P13A_KINASE_1; 1.
PROSTIE; P500915; P13A_KINASE_2; 1.
PNOSTIE; P500915; P13A_KINASE_2; 1.
PNOSTIE; P13A_KINASE_2; 1.
                                                                                             JOINED
EMBL; AJ297556; CAC21449.1; JG
EMBL; AJ297557; CAC21449.1; JG
EMBL; AJ297558; CAC21449.1; JG
EMBL; AJ297559; CAC21449.1; JG
EMBL; AJ297560; CAC21449.1; JG
PIR; AS4600; AS4600.
Genew; HGNC:8976; PIK3CB.
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50.0%;
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245 DYVLQVSGRVEYVF 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EYVIKVSARVRFFF 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-Sprague-Dawley;
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Local Similarity
nes 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APAH VIBCH
Q9KUS4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cholerae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACT SITE
SEQUENCE
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ACT SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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SO THE PRESENT OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     임
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                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib.cib.ch.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
                  PATHWAY: Signaling pathways regulating cell growth. SUBUNIT: HETERODIMER OF A P110 (CATALYTIC) AND A P85 (REGULATORY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable glutamine-dependent NAD(+) synthetase (EC 6.3.5.1) (NAD(+)
NADE OR TP0780.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98332770; PubMed=965876;
MEDLINE=98332770; PubMed=965876;
Praeer C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
Sodergren E., Hardhan J.M., McLeod M.P., Salzberg S., Peterson J.,
Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.
Machonald L., Arriach P., Bowman C., Cotton M.D., Fujii C., Garland
Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treponema pallidum.
Bacteria, Spirochaetes, Spirochaetales, Spirochaetaceae, Treponema
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51.2%; Score 41; DB 1; Length 1070; 50.0%; Pred. No. 11; 1; Indels tive 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1070 AA; 122607 MW; 4E8EB2333E96E4D5 CRC64;
                                                                                   SIMILARITY: Belongs to the PI3/PI4-kinase family.
                                                                                                                                                                                                                                                                                                                                         InterPro; 1FR008973; C2 C21B.
InterPro; 1FR008973; C2 C21B.
InterPro; 1FR000403; P13 P14 kinase.
InterPro; 1FR000403; P13 P14 kinase.
InterPro; 1FR000341; P13K_ras_bind.
InterPro; 1FR000341; P13K_ras_bind.
InterPro; 1FR000341; P13K_ras_bind.
InterPro; 1FR0001263; P13K_a.
Pfam; PF00494; P13K_C2; 1.
Pfam; PF00192; P13K_D85B; 1.
Pfam; PF00143; P13K p85B; 1.
SWART; SW00142; P13K C2; 1.
SWART; SW00144; P13K_rbd; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00915; PI3 4 KINASE 1; 1. PROSITE; PS00916; PI3 4 KINASE 2; 1. PROSITE; PS50290; PI3 4 KINASE 3; 1. Transferase; Kinase; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PI3K/PI4K
                                                                                                                                                                                                                                                                                                       EMBL; AJ012482; CAA10046.1; -. InterPro; IPR008938; ARM.
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245 DYVLQVSGRVEYVF 258
                                                                 (BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EYVIKVSARVRFFF 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00146; PI3Kc; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1050
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les 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Nichols;
                                                                 SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAINEEL TOR N16961, Serotype O1;

STRAINEEL TOR N16961, PubMed=10952301, 
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L., 
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A., 
Dodson R.J., Welson K.E., Read T.D., Tettelin H., Richardson D., 
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P., 
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O., 
Salzberg S.L., Smith H.O., Colwell R.R., Mekalancs J.J., Venter J.C., 
Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Bis (5-nucleosyl) -tetraphosphatase, symmetrical (EC 3.6.1.41)
(Diadenosine tetraphosphatase) (Ap4A hydrolase) (Diadenosine 5',5'''-
Pl,P4-tetraphosphate pyrophospholydrolase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --- FUNCTION: Hydrolyzes diadenosine 5',5'''-Pl,P4-tetraphosphate to yield ADP (By similarity).
                                                                                                                        -!- CATALYTIC ACTIVITY: ATP + deamido-NAD(+) + L-glutamine + H(2)O AMP + diphosphate + NAD(+) + L-glutamate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
spirochete.";
Science 281:375-388(1998).
-!- FUNCTION: CAN USE BOTH GLUTAMINE OR AMMONIA AS A NITROGEN
SOURCE (BY SIMILARITY).
                                                                                                                                                                                       -!- PATHWAY: NAD biosynthesis.
-!- SIMILARITY: In the C-terminal section; belongs to the NAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 40; DB 1;
Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGR; TP0780;

HAMAP; MF_0019; fused; 1.
InterPro; TPR03694; NAD synthase.
InterPro; IPR03010; Nt18c/CNhydtse.
Pfam; PF0240; NAD synthase; 1.
IIGRFAMs; TIGR00552; nadE; 1.
Ligaee; NAD; ATP-binding; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                269 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIGASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE001249; AAC65748.1; -. PIR; E71282; E71282.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     679 AA; 72152 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   649 VNLSPRVGFYFPS 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 IKVSARVRFFFPS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 406:477-483 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         383
                                                                                                                                                                                                                                                          synthetase family.
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InterPro; IPR000722; RNA pol A.
InterPro; IPR007080; RNA pol Rpbl 1.
InterPro; IPR007083; RNA pol Rpbl 3.
InterPro; IPR007083; RNA pol Rpbl 4.
InterPro; IPR007081; RNA pol Rpbl 5.
InterPro; IPR06592; RNA pol Rpbl 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21128732; PubMed=11234002;
                                                                                                                                 Pfam; PF04997; RNA DOI RDD1 1; 1.
Pfam; PF06623; RNA DOI RDD1 2; 1.
Pfam; PF05000; RNA DOI RDD1 3; 1.
Pfam; PF05000; RNA DOI RDD1 4; 1.
Pfam; PF04999; RNA DOI RDD1 4; 1.
SMART; SM00663; RPOLA N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U00013; AAA17119.1; -. EMBL; Z99125; CAB16170.1; -.
               EMBL; X96384; CAA65248.1;
HSSP; Q9KWU6; 1HQM.
                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 63.0
                                                                                                                                                                                                                                                                                                                                                                                    |||::|||:|
| || EYVLPISARLR 952
                                                                                                                                                                                                                                                                                                                                                                 1 EYVIKVSARVR 11
                                                                                                                                                                                                                                                          1004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium leprae.
                                                                                                                                                                                                                                                                         1004 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1769;
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ID YE62 MYCLE
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SEQUENCE
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                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Int. J. Syst. Bacteriol. 46:1004-1009(1996).
-!- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription of DNA into RNA using the four ribonucleoside triphosphates as
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
16-DNA-directed RNA polymerase beta' chain (EC.2.7.7.6) (Transcriptase beta' chain) (RNA polymerase beta' subunit) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97016803; PubMed=8863429;
Morse R., Collins M.D., O'Hanlon K., Wallbanks S., Richardson P.T.;
"Analysis of the beta' subunit of DNA-dependent RNA polymerase does
not support the hypothesis inferred from 16S rRNA analysis that
Oenococcus oeni (formetly Leuconostoc cenos) is a tachytelic
(fast-evolving) bacterium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  {RNA}(N).
-!- SUBUNIT: The enzyme consists of the sigma chain and the core enzyme which is composed of 2 alpha chains, 1 beta chain, and 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: Belongs to the RNA polymerase beta' chain family.
                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                              Length 269;
                                                                                                                                                                                                                                                                                                                                                                                               5; Indels
                                                                                                                                                                                                                                                                                                                  Hydrolase; Complete proteome.
SEQUENCE 269 AA; 30407 MW; B6D87AlC474D45BB CRC64;

    -!- SIMILARITY: Belongs to the Ap4A hydrolase family.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Lactobacillales; Oenococcus.
                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                             Query Match
48.8%; Score 39; D
Best Local Similarity 42.9%; Pred. No. 6;
                                                                                                                                                                                                       HAWAP; WF 200199; -; 1.
InterPro; IPR004611; ApaH.
InterPro; IPR004843; M-ppestrase.
InterPro; IPR006186; T_phtase_apaH.
Pfam; PP00149; Metallophos; 1.
TIGRFAMS; TIGR00668; ApaH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Denococcus oeni (Leuconostoc oenos)
                                                                                                                                                                                                                                                                                                                                                                                            3;
                                                                                                                                                             EMBL; AE004131; AAF93614.1; -. PIR; H82322; H82322.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        173 YIVNAFTRMRFCFP 186
                                                                                                                                                                                                                                                                                                                                                                                                                            2 YVIKVSARVRFFFP 15
                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      substrates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RPOC_OENOE
P95405;
                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor N. Holbavies R.M., Davlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L., Oliver K., Quall M.A., Rajandream M.A., Rutherford K.M., Rutherter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Barrell B.G.;
                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                         48.8%; Score 39; DB 1; Length 1004; 63.6%; Pred. No. 24;
                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                  111965 MW; 73750DF47F3A2C36 CRC64;
Transferase; DNA-directed RNA polymerase; Transcription.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Smith D.R., Robison K.;
Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein ML0594.
ML0594 OR MLCL536.27C OR U1496A OR B1496_C1_154.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Massive gene decay in the leprosy bacillus."; Nature 409:1007-1011(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-PEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                        3; Mismatches
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AL583919; CAC30102.1;

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                                                                                                             01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein in xynA 3'region (OFF6) (Fragment).
Caldicellulosiruptor sp. (strain ReBB.4).
Bacceria, Firmicutes; Clostridia; Clostridiales; Syntrophomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FARZ TEARLY SIMULAND; FRI; 100, A.P.
P19097; Q12533;
01-NOV-1990 (Rel. 16, Created)
10-NOV-1990 (Rel. 11, Last sequence update)
10-OCT-2003 (Rel. 42, Last sequence update)
11-100)
12-OCT-2003 (Rel. 42, Last sequence update)
13-OCC 2.3.1.41) (Beta-ketoacyl synthase)
13
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MEDLINE=88315020; PubMed=2900835;
Mohamed A.H., Chirala S.S., Mody N.H., Huang W.Y., Wakil S.J.;
Mohamed Y.H., Chirala G.S., Mody N.H., Huang W.Y., Wakil S.J.;
"Primary structure of the multifunctional alpha subunit protein of yeast fatty acid synthase derived from FAS2 gene sequence.";
J. Biol. Chem. 263:12315-12325(1988).
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDILINE=97077616; PubWed=8920183;
Divedi P.P., Gibbs M.D., Saul D.J., Bergquist P.L.;
Claiming, sequencing and overexpression in Escherichia coli of a xylanase gene, xynA from the thermophilic bacterium Rt8B.4 genus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     402 402
402 AA; 46442 MW; 5DSEC504960641F7 CRC64;
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Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              xylanase gene, xynA from the thermophilic bac
Caldicellulosiruptor.";
Appl. Microbiol. Biotechnol. 45:86-93(1996).
-!- SIMILARITY: SOME, TO M.GENITALIUM MG148.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1887 AA.
                                                               402 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L18965; AAB42046.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EYVIKVSARVRFFFPS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Ouery Coral Similarity 31.43,
Best Local Similarity 31.43,
Best Local Similarity 31.43,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                               STANDARD;
                                                                                                                                                                                                                                                                                     Caldicellulosiruptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; S41790; S41790.
Hypothetical protein.
NON TER 402 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                               NCBI_TaxID=28238;
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Schueller H.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
FAS2_YEAST
ID FAS2_YEAST
                                                               CALSR
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SEQUENCE
     RESULT 10
YORG CALSR
ID YORG CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- FUNCTION: Involved in the tonB-independent uptake of proteins (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAMAP; MF 00671; -; 1.
InterPro; IPR007195; TolB N.
Pfam; PF04052; TolB N, 1.
Transport; Protein transport; Periplasmic; Signal; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                           Gaps
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MEDLINE=20150912; PubMed=10688204;
Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
Whitehead S., Barrell B.G.;
"The genome sequence of the food-borne pathogen Campylobacter jejuni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Campylobacter jejuni.
Bacteria; Froteobacteria; Epsilonproteobacteria; Campylobacterales;
Campylobacteraceae; Campylobacter.
NCBI_TaxID=197;
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                                                                                                                                                                                              Score 38; DB 1; Length 392; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 402;
                                                                                                                                                                                                                                                     Indels
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                                              Deprome, MESS, UPF0051.

Pfam; PF01458; UPF0051, 1.

Hypothetical protein; Complete proteome.

SEQUENCE 392 AA; 42202 MW; 891162F7CA494C6A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TolB protein.
3E6178CE236B28A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SUBCELLULĀR LOCATION: Periplasmic (Potential).
                                                                                                                                                                                                                                                     3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
TOLB protein precursor.
                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47.5%; Score 38; 53.8%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 reveals hypervariable sequences.";
Nature 403:665-668(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AL139074; CAB72596.1; -.
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                                                                                                                                                                                              47.5%;
                                                                                                                                                                                                                                                                                                                                                             208 VVRVSANVRFSGP 220
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                                                                                                                                                                                                                                                                                                         3 VIKVSARVRFFFP 15
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                                                                                                                                                                                                                        Best Local Similarity 61.5
Matches 8; Conservative
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Matches 7; Conservative
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PIR; S72753; S72753.
Leproma; ML0594; -.
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Gaps

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Length 402; 4; Indels IIGRFAMS; TIGR00556; pantethn\_trn; 1.

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WEDLINE-9731327; PubMed-9169875;

WEDLINE-9731327; PubMed-9169875;

WEDLINE-9731327; PubMed-9169875;

WEDLINE-9731327; PubMed-9169875;

WEDLINE-9731327; PubMed-9169875;

WEDLINE-9731327; PubMed-9169875;

Bussey H., Storms R.K., Ahmed A., Albermann K., Allen E., Ansorge W., Bussey H., Storms B.C., Churcher C.M., Coster F., Davis R.W., Davis R.W.,

Dottstein D., Bowman S., Bruckner M., Cappenter J., Cherry J.M.,

Dottstein D., Bowman S., Hyman R., Davis R., Davis R.W.,

Dottstein B., Churcher C.M., Coster F., Davis R., Davis R.W.,

Hall J., Hebling U., Heumann K., Hilbert H., Hillier L.W.,

Hunicke Smith S., Hyman R., Johnston M., Kalman S., Kleine K.,

Marathe R., Messenguy F., Mewes H.-W., Mirtipati S., Moestl D.,

Marathe R., Messenguy F., Mewes H.-W., Mirtipati S., Moestl D.,

Marather S., Pohl T.W., Purnelle D., Schafer M., Schafe M.,

Scherens B., Schramm S., Schroeder M., Sdicu A.M., Tettelin H.,

Urrestarazu L.A., Ushinsky S., Vierendeels F., Vissers S., Voss H.,

Walsh S.V., Wamputt R., Wang Y., Wedler E., Wedler H., Winnett E.,

Zhong W.W., Zollner A., Vo D.H., Hani J.;

"The nuclecides esquence of Saccharomyces cerevisiae chromosome XVI.";

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            altered fatty acid synthase gene.";

Mol. Gen. Genet. 244:90-96(1994).

-!- FUNCTION: Fatty acid synthase gene.";

non-chain fatty acid synthase catalyzes the formation of the alpha subunit contains domains for: acyl carrier protein. The alpha subunit contains domains for: acyl carrier protein] reductase, and 3-oxoacyl-[acyl-carrier protein] reductase, and 3-oxoacyl-[acyl-carrier-protein] synthase. This subunit coordinates the binding of the six beta subunits to the enzyme complex.

-!- CATALYTIC ACTIVITY: Acetyl-CoA + N Malonyl-CoA + 2N NADPH = a long-chain acyl-CoA + N COA + N N NADPH.

-!- CATALYTIC ACTIVITY: Acetyl-carrier protein] + malonyl-[acyl-carrier protein] = 3-oxoacyl-[acyl-carrier protein] + co(2) + carrier protein] = 3-oxoacyl-[acyl-carrier protein] + malonyl-(acyl-carrier protein] + nalonyl-carrier protein] + NADPH.

-!- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] + NADPH.

-!- SUBUNIT: [Alpha (6) beta (6)] hexamers of two multifunctional subunits (alpha and beta).

-!- SIMILARITY: TO THE FATTY ACID SYNTHETASE, SUBUNIT ALPHA FROM OTHER FUNGI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=S288c;
MEDLINE=94316198; PubMed=8041367;
Inokoshi J., Tomoda H., Hashimoto H., Watanabe A., Takeshima H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Cerulenin-resistant mutants of Saccharomyces cerevisiae with an
Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGD; S0006152; PAS2.
InterPro; IPR008278; 4-PPT_transf.
InterPro; IPR000794; Ketoacyl synth.
InterPro; IPR004568; Pantethn_trn.
InterPro; IPR004662; Ppantne_S.
Pfam; PF01648; ACPS; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00109; ketoacyl-synt; 1.
Pfam; PF02801; ketoacyl-synt_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; J03936; AAA34601.1; --
EMBL; X76890; CAA54218.1; --
EMBL; X94561; CAA64256.1; --
EMBL; Z73586; CAA97947.1; --
EMBL; Z73586; CAA97947.1; --
PIR; S61703; S61703; GAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 387:103-105(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MUTAGENESIS OF GLY-1250.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Omura S.;
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                                                                                                               BETA-KETOACYL REDUCTASE.
BETA-KETOACYL REDUCTASE.
BETA-KETOACYL SYNTHASE.
PHOSPHOPANTETHEINE (BY SIMILARITY).
BETA-KETOACYL SYNTHASE (BY SIMILARITY).
G-S: CERULENIN-RESISTANCE.
G -> CTTGTGG (IN REF. 1).
T -> I (IN REF. 1).
T -> I (IN REF. 1).
CLOCKSWLKLIKLERQEPSKLIMSIRLSMAIALHHLKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; Short J.M., In the complete genome of the hyperthermophilic bacterium Aquifex
               PROSITE; PS00012; PHOSPHOPANTĒTHEINB; 1.
PROSITE; PS00606; B KETOACYL SYNTHASE; 1.
Fatty acid biosynthēsis; Mulēifunctional enzyme; Oxidoreductase;
Transferase; NADP; Phosphopantetheine.
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Pred. No. 73;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            RWEMEA -> KMGNGS (IN REF. 1).
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E2ADC83776605AE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1408 1408 A -> S (IN REF. 1).
1671 1671 N -> T (IN REF. 1).
1887 AA; 206946 MW; 08B872734CF3AEEA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
NCBI_TaxID=63363;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein AQ_1854 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98196666; PubMed=9537320;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47.5%;
58.8%;
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Best Local Similarity 63.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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1408
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Best Local Similarity
Local 10; Conserva
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1408
1671
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16-OCT-2001
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ID YIS4_AQUAE
AC O67706;
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                                                                                                                                                                                                                                                                                                                                                                                                   Buell C.R., Joardar V., Lindeberg M., Selengut J., Paulsen I.T.,
A Gwinn M.L., Dodson R.J., Deboy R.T., Durkin A.S., Kolonay J.F.,
A Madupu R., Davidsen T., Zefar N., Zhou L., Liu J., Yuan Q.,
Nelson W.C., Davidsen T., Zafar N., Zhou L., Liu J., Yuan Q.,
A Khouri H., Fedorova N., Tran B., Russell D., Berry K., Utterback T.,
A na Aken S.E., Feldblyum T.V., D'Ascenco M., Deng W.-L., Ramos A.R.,
A Alfano J.R., Cartinhour S., Chatterjee A.K., Delaney T.P.,
A mazrowitz S.G., Martin G.B., Schneider D.J., Tang X., Bender C.L.,
White O., Fraser C.M., Collmer A., A., Arabidopsis and tomato pathogen
T Pseudomonas syringae pv. tomato DC3000.";
Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186(2003).
C-!- CATALYTIC ACTIVITY: ATP + L-aspartate + tRNA(Asp) = AMP +
C. HINDSPHAE H. L-aspartyl-tRNA(Asp).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HAMAP; MF-00044; -; 1.
InterPro; IPR004115; GAD dom.
InterPro; IPR004115; CAD dom.
InterPro; IPR004135; TRNA-synt_asp.
InterPro; IPR004365; TRNA_anti.
InterPro; IPR004365; TRNA_anti.
InterPro; IPR004365; TRNA_anti.
Pfam; PF02938; GAD; 1.
Pfam; PF00135; TRNA_anti; 1.
Pfam; PF00136; TRNA_anti; 1.
PRINTS; PR01042; TRNA_ANTIHASP.
PROSTTE; PS080862; AA_TRNA_LIGASE II; 1.
Aminoacy1-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBUNIT: Homodimer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
                                                                             15-WAR-2004 (Rel. 43, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Aspartyl-tRNA synthetase (BC 6.1.1.12) (Aspartate--tRNA ligase)
                                                                                                                                                                                                  Pseudomonas syringae (pv. tomato).
Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales,
       591 AA
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                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22834015; PubMed=12928499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE016870; AAO57440.1; -. TIGR; PSPT03981; -.
                                                 15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last seq
15-MAR-2004 (Rel. 43, Last ann
                                                                                                                                                                                                                                                              Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 63.6
Matches 7; Conservative
     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EYVIKVSARVR 11
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                                                                                                                                                                 (ABPRS).
ASPS OR PSPTO3981.
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SEQUENCE 591 AA
                                                                                                                                                                                                                                                                                   NCBI_TaxID=323;
     SYD PSESM
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                            Q87<u>Y</u>31;
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GAAT_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kim K., Kim K.-H., Storey M.K., Voelker D.R., Carman G.M.;
"Isolation and characterization of the Saccharomyces cerevisiae EKII gene encoding ethanolamine kinase.";
J. Blod. Chem. 274:14857-14866(1999)
-1- FUNCTION: Catalyzes the committed step of phosphatidylethanolamine synthesis via the CDP-ethanolamine pathway. Also exhibits choline kinase activity but its preferred substrate is ethanolamine.
-1- CATALYTIC ACTIVITY: ATP + ethanolamine = ADP + O-phosphoethanolamine.
-1- PATHWAY: Phosphatidylethanolamine biosynthesis.
-1- SIMILARITY: Belongs to the choline/ethanolamine kinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=S288c / AB972;
Murphy L., Richards C., Harris D., Barrell B.G., Rajandream M.A.,
Walsh S.V.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                       30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last sencence update)
Ethanolamine kinase (EC 2.7.1.82) (EK).
EKII OR YDB147W OR YD8358.04.
EXII OR YDB147W OR YD8358.04.
Eukaryota; Rungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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SGD; S0002554; EKI1.

GO; GO:0004103; F:choline Kinase activity; IDA.

GO; GO:0004103; F:choline Kinase activity; IDA.

GO; GO:000646; P:phosphatidylethanolamine biosynthesis; IMP.

InterPro; IPR005521; Choline kin N.

InterPro; IPR005531; Choline kinase.

Pfam; PF04428; Choline kin N; 1.

Pfam; PF01633; Choline kinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46.2%; Score 37; DB 1; Length 534; 53.8%; Pred. No. 30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47B417841D5005A8 CRC64;
                                                                                                                                                                              534 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99262638; PubMed=10329685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               534 AA; 61657 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Z50046; CAA90370.1; -.
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Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                              STANDARD;
5 KVSARVRFFFP 15
                                                 68 EVSÁRVKKFYP 78
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GermOnline; 140638;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4932;
                                                                                                                                                                           EKI1 YEAST
003764;
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SEQUENCE
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                                46.2%; Score 37; DB 1; Length 591; 63.6%; Pred. No. 33; ive 2; Mismatches 2; Indels
591 AA; 66351 MW; 4A841555305FBF36 CRC64;
                                                                                                                                                                                                                                           632 AA.
                                                                                                                                                                                                                                       GAAT HUMAN STANDARD; I
Q9UNB8; Q9NZK8;
16-OCT-2001 (Rel. 40, Created)
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RESULT 14

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=20266167; PubMed=10804200;
Sinkkonen S.T., Hanna M.C., Kirkness E.F., Korpi E.R.;
GABAA receptor epsilon and theta subunits display unusual structural variation between species and are enriched in the rat locus
                                                                                                                                                                                                                                                                                                                                                                                                                         ceruleus.";
J. Bukrosci. 20:3588-3595(2000).
J. Bukrosci. 20:3588-3595(2000).
-!- PUNCTION: GABA, the major inhibitory neurotransmitter in the vertebrate brain, mediates neuronal inhibition by binding to the GABA/benzodiazepine receptor and opening an integral chloride
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
GAMMA-AMINOBUTYRIC-ACID RECEPTOR THETA
                                                                                                                                                                                   SEQUENCE OF 6-632 FROM N.A.

BEDLINE-99380615. PubMed=10449790;

BODNERT T.P., McKernan R.M., Farrar S., le Bourdelles B.,

Heavens R.P., Smith D.W., Hewson L., Rigby M.R.,

Stintanthainghij D.J.S., Brown N., Waffford K.A., Whiting P.J.;

"Theta, a novel gamma-aminobuvyric acid type A receptor subunit.";

Proc. Natl. Acad. Sci. U.S.A. 96:9891-9896(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   channel.
--- SUBUNT: Generally pentameric. This subunit coassembles with alpha-2, beta-1 and gamma-1.
--- SUBCELLULAR LOCATION: Integral membrane protein.
--- SIMILARITY: Belongs to the ligand-gated ionic channel family.
                                                                      Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates; Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Gamma-aminobutyric-acid receptor theta subunit precursor (GABA(A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R MIM; 300349; -.

R GO; GO:0005887; C:integral to plasma membrane; TAS.

R GO; GO:0005326; F:neurotransmitter transporter activity; TAS.

R GO; GO:0004165; F:neignal transduction; TAS.

R GO; GO:0007165; P:signal transduction; TAS.

R InterPro; IPR008101; GABAAC receptor.

R InterPro; IPR006202; Neur_chanel.memb.

R InterPro; IPR006202; Neur_chan.LBD.

R InterPro; IPR006202; Neur_chan.LBD.

R Pfam; PF02331; Neur_chan.LBD; 1.

R Pfam; PF02331; Neur_chan.memb; 1.

R PRINTS; PR01725; GABARTHETA.

R PRINTS; PR01725; GABARTHETA.
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BY SIMILARITY.
N-LINKED (GLCNAC. .) (POTENTIAL).
F -> I (IN REF. 2).
C13267AC9212118B CRC64;
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PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
Postsynaptic membrane; Ionic Channel; Glycoprotein; Signal; Multigene family; Transmembrane; Chloride channel.
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EMBL; AF189259; AAF70380.1; -.
Genew; HGNC:14454; GABRQ.
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269
327
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632 AA;
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MIM; 300349;
                                                           receptor).
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         Score 37; DB 1; Length 632; Pred. No. 36; Mismatches 6; Indels
                             1,
Query Match
Best Local Similarity 53.39
Conservative
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602 DÝVPKVDKWSŘFLFP 616

Search completed: October 7, 2004, 15:14:00 Job time : 11.9091 secs

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Q88z80 lactobacill
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                           61M660
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Sui Y., Ye J., Wu W.;
"Cloning of a new gene of MAGE family in human hepatocellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Length 316;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     carcinoma.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; A443295, AA137997.1; -.
Inter'Proj.1FR001190; WAGE.
Pfam; PF01454; MACE; 1.
PROSITE; PS50838; MAGE; 1.
SEQUENCE 316 AA; 35409 MW; A463A9A740A089DF CRC64;
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Last annotation update)
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                                                                                                                                                  Q9VTB5
Q8MPP0
Q9RMZ5
Q8KYF2
Q8P1N0
Q9XE32
Q9XCM2
Q9XVM2
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Q8Y8D6
Q9C6A2
Q84WG3
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                        Q99WV9
Q8NYG9
O42291
Q81VY0
Q81J87
Q8MPN9
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09TCB6
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09 DHN9
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Q84M44
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Q8WWH6;
01-MAR-2002 (TFEMBLrel. 20
01-MAR-2003 (TFEMBLrel. 20
01-MAR-2003 (TFEMBLrel. 22
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Best Local Similarity 100.
Matches 16; Conservative
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Homo sapiens (Human).
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    RESULT 2
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097019 halocynthia
QBrx05 arabidopsis
QBcff1 mus musculu
QBr624 fusobacteri
QBr624 fusobacteri
QBr826 bacillus an
QBRei5 chlorobium
QBF931 leptospira
QBF931 leptospira
QBU304 agrobacteri
QB122 campylobact
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Q93n48 coxiella bu
Q14798 homo sapien
Q9bun9 homo sapien
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                                                                                                                                              October 7, 2004, 15:14:05 ; Search time 57.8182 Seconds (without alignments) 87.313 Million cell updates/sec
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                      GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Q94N9
Q9FUN9
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Q87019
Q8RK05
Q8RE21
Q8BT19
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Q8F9W3
Q8F9W3
Q8F9W3
Q8F9W3
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1: Sp archea:*
2: sp_bacteria:*
3: sp fung1:*
4: sp_human:*
5: sp_invertebrate:*
5: sp_mammal:*
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Gapop 10.0 , Gapext 0.5
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sp_virus:*
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Indels

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Cyprinus carpio (Common carp).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Cyprinus.
NCBI_TaxID=7962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S., Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Phelan M., Farmer A.; "Cloning of human full-length CDSs in BD Creator (TM) System Donor
                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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"Molecular cloning of a carp Jak3 from activated leukocytes.";
Vet. Immunol. Immunopathol. 74:225-236(2000).
EMBL; AF148993; AAF24169.1;
HSSP; Pl1362; 1FGK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 318;
                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Skin antigen, family A, 8 (Melanoma antigen, family A, 8).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Skin;
Strausberg R.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vector.";
Submitted (MAY_2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC002455, AAH02455.1; -.
EMBL; BC012744; AAH12744.1; -.
EMBL; BT007340; AAP36004.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        318 AA; 35214 MW; EA02C1FB42F6C080 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                      5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63.7%; Score 51; DB 4; 56.2%; Pred. No. 0.31;
  Pred. No. 0.31;
                                                                                                                                                                                                     318 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1126 AA.
                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0005856; C:cytoskeleton; IEA
                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20264065; PubMed=10802290;
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2
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289 EHVVRVNARVRIAYPS 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 291 EHVVRVNARVRISYPS 306
56.2%;
                                                            1 EYVIKVSARVRFFFPS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EYVIKVSARVRFFFPS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002190; MAGE.
Pfam; PF01454; MAGE; 1.
PROSITE; PS50838; MAGE; 1.
                      9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; Conservative
                                                                                                                                                                                                     PRELIMINARY;
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  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Koi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                          Q9BUN9;
                                                                                                                                                                                                     9BUN9
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                      Matches
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Q9PTN6
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                                                                                                                                                                                               Hoover T.A., Vodkin M.H., Williams J.C., Culp D.W., Thompson H.A.; "A chromosomal DNA deletion explains the phenotype of the Coxiella burnetii phase II variant.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAGE-4 protein.
MELANOMA ANTIGER-4.
HOMO Sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                             STRAIN-Nine Mile phase I / RSA 493;
MEDLINE-22608657; PubMed=12704232;
Seshadri R., Paulsen I.T., Eisen J.A., Read T.D., Nelson K.E.,
Selson W.C., Mard N.L., Tettelin H., Davidsen T.M., Beanan M.J.,
DeBoy R.T., Daugherty S.C., Brinkac L.M., Madugu R., Dodson R.J.
Khouri H.M., Lee K.H., Caxty H.A., Scanlan D., Heinzen R.A.,
Thompson H.A., Samuel J.E., Fraser C.M., Heidelberg J.F.;
"Complete genome sequence of the Q-fever pathogen, Coxiella
burnetii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE-95369706; PubMed=7642112; MEDLINE-95369706; PubMed=7642112; Imai Y., Shichijo S., Yamada A., Katayama T., Yano H., Itoh K.; Sequence analysis of the NAGE gene family encoding human tumor-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
0
                                                                CBUOUSS.
Bacteria, Proteobacteria, Gammaproteobacteria, Legionellales,
Coxiellaceae, Coxiella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65.0%; Score 52; DB 16; Length 458; ilarity 56.2%; Pred. No. 0.28; Conservative 5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 317;
                                                                                                                                                                                                                                                           (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein; Complete proteome.
SEQUENCE 458 AA; 53179 MW; A42FF461553D648 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35044 MW; 9B9477253FE307C4 CRC64;
19, Last sequence update)
24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 100:5455-5460(2003).
EMBL; AE016962; AAC90239.1; -.
TIGR; CBU0695: -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIGR; CBU0695; -.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0016118; F:oelectron transport; IEA.
InterPro; IPR065797; Cytb. b6 N.
PROSITE; PS00192; CYTOCHRÖME_B.HEME; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rejection antigens.";
Gene 160:287-290(1995).
EMBL; D32075; BAA06841; -
InterPro; IPR002190; MAGE.
Pfam; PF01454; MAGE; 1.
PROSITE; PS50839; MAGE; 1.
SEQUENCE 317 AA; 35044 PW;
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01-NOV-1996 (TrEMBLrel. 01,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
01-DEC-2001 (TrEMBLrel. 01-JUN-2003 (TrEMBLrel.
                                     Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 9, Conserv
                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                         NCBI_TaxID=777;
                                                                                                                                                                                                                                                             Submitted
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RESULT 3 Q14798

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Gaps

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53.8%;
50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51.2%;
                                                                                                                                   |:| :| :||||
375 YIIDMSRSAKFPFP 388
                                                     Query Match
Best Local Similarity 50.vv.
Best and 7; Conservative
                                                                                                                   2 YVIKVSARVRFFFP 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183 IYKVSVLVRLFFP 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 VIKVSARVRFFFP 15
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nes 8; Conservative
                                                                                                                                                                                                          PRELIMINARY;
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MEDLINE=99101502; PubMed=9886411;
MODAKA M., Azumi K., Ji X., Namikawa-Yamada C., Sasaki M., Saiga H.,
Dodds A.W., Sekine H., Homma M.K., Mateushita M., Endo Y., Fujita T.;
"Opsonic_complement component C3 in the solitary ascidian, Halocynthia
                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                               ö
GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.

GO; GO:000742; P:intransferase activity; IEA.

GO; GO:000742; P:intransferase activity; IEA.

GO; GO:000742; P:intracellular signaling cascade; IEA.

GO; GO:0006469; P:protein amino acid phosphorylation; IEA.

InterPro; IFR000299; Band 4.1.

InterPro; IFR000199; Band 4.1.

InterPro; IFR000199; SH2.

InterPro; IFR000145; Tyr pkinase.

InterPro; IFR000145; Tyr pkinase.

Pfem; PP00017; SH2; 1.

RFMNTY; PR00109; TYRKINASE.

ProDom; PD0000091; Proc. kinase; 2.

ProDom; PD0000091; Proc. kinase; 2.

ProDom; PD0000091; Proc. kinase; 2.
                                                                                                                                                                                                                                                                                                                                    56.2%; Score 45; DB 13; Length 1126; 76.9%; Pred. No. 14; ive 0; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                ATP-binding, Kinase, Transferase, Tyrosine-protein kinase.
SEQUENCE 1126 AA; 129335 MW; BCF94D35F76C411D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0005576; C:extracellular; IEA.
GO; GO:0003779; F:actin binding; IEA.
GO; GO:0004866; P:endopeptidase inhibitor activity; IEA.
InterPro; IPR002890; A2M N.
InterPro; IPR001589; Actbind_actnin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Halocynthia roretzi (Sea squirt).
Eukaryota, Metazoa, Chordata, Urochordata, Ascidiacea,
Stolidobranchia, Pyuridae, Halocynthia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1740 AA
                                                                                                                                                                                            SMART; SM00295; B41; 1.
SWART; SM00229; B12; 1.
PROSITE; PSS0019; TYPKC; 1.
PROSITE; PSS00107; PROFEIN XINASE ATP; 1.
PROSITE; PSS00117; PROFEIN XINASE DM; 2.
PROSITE; PSS00119; PROFEIN XINASE DM; 2.
PROSITE; PSS00119; SM2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR009048; AM receptor bind. InterPro; IPR000020; Anaphylatoxin. InterPro; IPR0011599; MacroglobinA2. InterPro; IPR001134; Netrin_C. InterPro; IPR008930; Terp_cyc_toroid. Pfam; PF00207; A2M; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          roretzi.";
J. Immunol. 162:387-391(1999).
EMBL; mAD006564; BAA75069.1; -.
HSSP; P01024; IC3D.
                                                                                                                                                                                                                                                                                                                                                                                                               95 IKVHYRVRFFFSS 107
                                                                                                                                                                                                                                                                                                                                                                                        4 IKVSARVRFFFPS 16
                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 76.9
Matches 10; Conservative
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Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,

A Dang J.M., Goldmaith A.D., Lee J.M., Onodera C.S., Quach H.L.,

A Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,

Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,

Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,

Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,

A Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K.,

A Davis R.W., Ecker J.R., Theologis A.;

"Arabidopsis Full Length CDNA Clones.";

Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AY090996; AAM14019.1;

"Whypotherical protein."
                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ol-car-zous (TrEMBLrel. 23, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to phosphatidylinositol 3-kinase, catalytic subunit, beta
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                                                                                                                                                                     Score 43; DB 5; Length 1740;
Pred. No. 51;
3; Mismatches 4; Indels
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SMART; SM00643; C345C; 1.
PROSTIE; PS00019; ACTININ 1; 1.
PROSTIE; PS00477; ALPHA 2 MACROGLOBULIN; 1.
SEQUENCE 1740 AA; 196070 MW; 12AB150CDF3B3333 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC039650; AAH39650.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       246 AA; 28058 MW; 0159187F22D4255E CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment).
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1; Mismatches
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Fri Oct

RESULT 10

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RC TISSUES-COlon;

RX MEDLINE-22354683; PubMed=12466851;

RA The FANTOM COnscrtium,

The RIKEN Genome Exploration Research Group Phase I & II Team;

The RIKEN Genome Exploration Research Group Phase I & II Team;

RT "Analysis of the mouse transcriptome based on functional annotation of RT "Analysis of the mouse transcriptome based on functional annotation of RT "Analysis of the mouse transcriptome based on functional annotation of RT "Analysis of the mouse transcriptome based on functional annotation of RT "Analysis of the mouse transcriptome based on functional annotation of RT "Analysis of the mouse transcriptome based on functional annotation of RT "Analysis of the mouse transcriptome based on functional annotation of RT "Analysis of PRAS" | "C CalB."

DR MGD; MGI:1922019; PiRAS.

DR InterPro; IPR000493; PISK.

DR InterPro; IPR000493; PISK.

DR InterPro; IPR000493; PISK.

DR InterPro; IPR000493; PISK.

DR Fam; PF00194; PISK.

DR Fam; PF00194; PISK.

DR Fam; PF00454; PISK.

DR Fam; PF00454; PISK.

DR Fam; PF00455; PISK.

DR SWART; SW00145; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
P15D2.32.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi; Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51.2%; Score 41; DB 11; Length 1064; 50.0%; Pred. No. 76; 3; Indels (ative 4; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWART; SW00142; PI3K_C2; 1.
SWART; SW00143; PI3K_D895; 1.
SWART; SW00144; PI3K_D895; 1.
PROSITE; PS00915; PI3_4_KINASE_1; 1.
PROSITE; PS00916; PI3_4_KINASE_2; 1.
PROSITE; PS00290; PI3_4_KINASE_3; 1.
SRQUENCE 1064 AA; 121753 MW; 3E96729B25C52DIC CRC64;
                                                                                                                                                01-0CT-2003 (TrEMBLrel. 25, Last sequence update) Phosphatidylinositol 3-kinase catalytic subunit. PIK3CB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09C703;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                           PRT; 1064 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 132 AA
                                                                                                                                    Created)
                                                                                                                                 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :||::|| || : |
239 DYVLQVSGRVEYVF 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EYVIKVSARVRFFF 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 50.0
                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN=cv. Columbia;
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
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                                                                                                                                    01-MAR-2003
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                                                                  Q8BTI9
Q8BTI9;
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Q9C7Q9
                                             Q8BTI9
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SEQUENCE FROM N.A.

SEQUENCE 25586;

RA MEDINE-21865394; PubMed-11889109;

RA MEDINE-21865394; PubMed-11889109;

RA SABATRAL V. Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,

RA Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,

RA Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,

RA Jersen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,

RA Larsen M., Kyrpides N., Overbeek R.;

RA Fonstein M., Kyrpides N., Overbeek R.;

RY "Genome sequence and analysis of the oral bacterium Fusobacterium

RY "Genome sequence and analysis of the oral bacterium Fusobacterium

RY "Genome sequence and analysis of the oral bacterium fusobacterium

RY "Genome sequence and analysis of the oral bacterium fusobacterium

RY "Go (00:001678); F.:6-adenosylmethionine-dependent methyltransf. ..; IEA.

BY GO; GO:0016740; F.:1aransferase activity; IEA.

GO; GO:0016740; F.:1aransferase activity; IEA.

GO; GO:0016740; F.:a-denosylmethionine-dependent methyltransf. ..; IEA.

RITERPRO; IPRO00051; SAM bydrolase.

InterPro; IPRO00051; SAM bydrolase.

RY Transferase: Methyltransferase; Complete proteome.

RY Fransferase: Methyltransferase; Complete proteome.

SEQUENCE 566 AA; 66044 MW; 59FBC45E012BF858 CRC64;
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R GO; GO:0005942; C:1-phosphatidylinositol 3-kinase complex; IEA.
R GO: GO:0016301; F:kinase activity; IEA.
GO; GO:0016301; F:kinase activity; IEA.
R GO; GO:0007165; P:signal transduction; IEA.
R InterPro; IPR008973; C2 Calb.
InterPro; IPR008973; C2 Calb.
R InterPro; IPR008973; C2 Calb.
R InterPro; IPR00131; PI3K_D51.
R Pfam; PF00792; PI3K_C2; I.
R Pfam; PF00794; PI3K_C2; I.
R Pfam; PF00794; PI3K_D65B; I.
R SMART; SM00142; PI3K_D65B; I.
R SMART; SM00144; PI3K_D65; I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 51.2%; Score 41; DB 11; Length 409; Best Local Similarity 50.0%; Pred. No. 31; Matches 7; Conservative 4; Mismatches 3; Indels
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Pred. No. 42;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fusobacterium nucleatum (subsp. nucleatum).
Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
Fusobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        409 AA; 46976 MW; 5545E974376E45D3 CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-GCT-2003 (TrEMBLrel. 25, Last annotation update)
Methyltransferase (EC 2.1.1..).
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Best Local Similarity 61.5%;
Matches 8; Conservative
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239 DYVLQVSGRVEYVF 252
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SEQUENCE
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Q8R624;
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RESULT 9 Q8R62

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Gaps

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EMBL; AE011199; AAN47273.1; -.
Hypothetical protein; Complete proteome.
                        3 VIKVSARVRFFFP 15
                                                   ::|:::: | |||
51 ILKIASKFRMFFP
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                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1097;
                                                                                                                                                                                                                                                                                                                                                                                                      Chlorobium.
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                                                                                                                                          RESULT 13
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              Theologis A., Ecker J.R., Falm C.J., Federspiel N.A., Kaul S.,
Mite O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
Chung M.K., Con L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
Chung M.K., Con L., Jenkins J., Hansen N.F., Hughes B., Huizar L.,
A dill J.E., Goldsmith A.D., Hass B., Hansen N.F., Hughes B., Huizar L.,
A kim C.J., Jenkins J., Johnson-Hopson C., Khan S., Khaykin B.,
Langin-Hooper S., Lee A., Johnson-Hopson C. A., Li J.H., Li Y.-P.,
Lin X., Liu S.X., Liu Z.A., Lucso J.S., Maiti R., Marziali A.,
Langin-Hooper S., Lee J.M., Nguyen M., Nerman W.C., Osborne B.I.,
Rim G.J., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
Sakano H., Salzerg S.L., Schwatz J.R., Shinn P., Southwick A.M.,
Sakano H., Salzerg S.L., Schwatz J.R., Shinn P., Southwick A.M.,
W. D., Yu G., Fraser C. W., Venter J.C., Davis R.W.;
"Herback T., Van Aken S., Vaysberig M., Vysotskaia V.S., Walker M.,
"House J. W. G., Fraser C. W., Venter J.C., Davis R.W.;
"Sequence and analysis of Chromosome I of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22608414; PubMed=12721629;
Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T.,
Nelson K.E., Tettelin H., Fouts D.E., Bisen J.A., Gill S.R.,
Holtzapple E.K., Okstad O.A., Helgason E., Rilstone J., Wu M.,
Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.,
DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L.,
Thomason B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.0%; Score 40; DB 10; Length 132; 50.0%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus anthracis (strain Ames).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ll protein.
132 AA; 15103 MW; P516C550FF585A11 CRC64;
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201 AA; 24202 MW; 21B0CBAB1E30FB62 CRC64;
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
MEDLINE=21016719; PubMed=11130712;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AC068667; AAG51732.1; -. PIR; H86416; H86416.
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(TrEMBLrel. 24, L
(TrEMBLrel. 24, L
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36 FVVYTSDRIRFAFP 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 50.0 Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 408:816-820(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 423:81-86(2003)
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI TaxID=198094;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                            thaliana.";
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STRAIN=TLS / ATCC 49652 / DSM 12025;
MEDLINE=22103685; Pubmed=12039301;
A Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,
Dodson R.J., Deboy R., Gwinn M.L., Nelson W.C., Haft D.H.,
Hickey B.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F.,
A Holt I., Umayam L.A., Mason T., Brenner M., Shea T.P., Parksey D.,
A Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune D.,
A veneta J.C., Tettellih H., Bryant D.A., Praser C.M.;
The complete genome sequence of Chlorobium tepidum TLS, a
photosynthetic, anaerobic, green-sulfur bacterium.";
B. Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514 (2002).
R. TIGR; CT0704; -
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                                                                                                                                                         Chlorobium tepidum.
Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
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Pred. No. 30;
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STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
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                                                                    Last sequence update)
Last annotation update)
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Last sequence update)
Last annotation update)
248 AA
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                                           Created)
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23,
                                       Protease; Complete proteome
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nes 7; Conservative
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14 EYTVKVSQRARY 25
PRELIMINARY;
                                                                                                                     Zinc protease, putative.
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01-MAR-2003 (TrEMBLrel.
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WEDLINE-21608550; PubMed-11743193;

WEDLINE-21608550; PubMed-11743193;

WOOD D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,

Nokura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,

Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,

Chapman P., Clendenning J., Datherage G., Gillet W., Grant C.,

Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,

A Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,

Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,

A Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,

Nester E.W.;

T. The genome of the natural genetic engineer Agrobacterium tumefaciens
T. 558.";
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MEDLINE=21608551; PubMed=11743194;
MEDLINE=21608551; PubMed=11743194;
MOOder B., Hinkle G., Gattung S., Miller N., Blanchard M.,
Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
Holmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
Mollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
Cielo C., Slater S.;
Geneme sequence of the plant pathogen and biotechnology agent
Agrobacterium tumefaciens C.88.";
Science 294:2323-2328(2001).
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
1-JUN-2003 (TrEMBLrel. 24, Last annotation update)
ATU3824 OR AGR L_2017.
Agrobacterium Tumefaciens (strain CSS / ATCC 33970).
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales;
Rhizobiaceae, Rhizobium/Agrobacterium group; Agrobacterium.
NCBI_TAXID=17629;
                       / Match 50.0%; Score 40; DB 16; Length 264; Local Similarity 58.3%; Pred. No. 31; Conservative 2; Mismatches
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EMBL; AE008301; AAK89584.1; -.
PIR; AD3027; AD3027.
PIR; F98257; F98257.
Hypothetical protein; Complete proteome.
SEQUENCE 327 AA; 38174 MW; FFE53F6F9EAEB8E3 CRC64;
264 AA; 29314 MW; 818D15A61E4BC22A CRC64;
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Best Local Similarity 46.74
Matches 7; Conservative
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Search completed: October 7, 2004, 15:16:59 Job time: 59.8182 secs

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October 7, 2004, 12:53:09 ; Search time 47.1818 Seconds (without alignments) 71.862 Million cell updates/sec
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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                                                                           - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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57
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. geneseqp2004s:\*

IES	Description	Aab31295 Peptide d	Aab31291 Peptide d	Aab31292 Peptide d	Aau85042 Human MAG	Aar70909 Human mel	Aaw81548 Tumour re	Aab31290 Amino aci	Aae06806 Human MAG	Aau84814 Human MAG	Abp74195 Human MAG	Abu08930 Human tum	Adc09573 MAGE-1 pr	Aao19742 Wild-type	Abu04419 Human exp	AAY06592 CLYTA-MAC	Aay06590 Lipoprote		Aau85130 Human me	Aay38326 MAGE-deri	Aar70948 Human me]	Aar70960 Human me	Aay46118 Immunogen	Aay45907 Immunogen	Abp74245 Human MAG	
SUMMARIES	11	AAB31295	AAB31291	AAB31292	AAU85042	AAR70909	AAW81548	AAB31290	AAE06806	AAU84814	ABP74195	ABU08930	ADC09573	AA019742	ABU04419	AAY06592	AAY06590	ABR57354	AAU85130	AAY38326	AAR70948	AAR70960	AAY46118	AAY45907	ABP74245	
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Aar70953 Human mel	Aay46179 Immunogen	Aar70957 Human mel	Aar70966 Human mel	Aay46178 Immunogen	Aar73839 Antigen f	Aar78916 MAGE 1 28	Aar70923 Human mel	Aay47412 Immunogen	Aab98466 HLA class	Aag84522 Human leu	Aau06282 Human Leu	Aag88274 Human leu	Aag89370 Human leu	Aaj00058 Hepatitis	Abb78054 Amino aci	Aae31181 Human mag	Abb99586 Peptide M	Aau85043 Human MAG	Ada34084 Acinetoba
AAR70953	AAY46179	AAR70957	AAR70966	AAY46178	AAR73839	AAR78916	AAR70923	AAY47412	AAB98466	AAG84522	AAU06282	AAG88274	AAG89370	AAJ00058	ABB78054	AAE31181	ABB99586	AAU85043	ADA34084
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78.9	78.9	73.7	73.7	73.7	71.9	71.9	71.9	71.9	71.9	71.9	71.9	71.9	71.9	71.9	71.9	71.9	71.9	71.9	71.9
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56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	. 41	42	43	44	45

## ALIGNMENTS

RESULT 1

AAB3129

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A Geneseq 29Jan04:\* 1: geneseqp1980s:\* 2: geneseqp1990s:\*

Database :

geneseqp20028:\* geneseqp2003a8:\* geneseqp2003bs:\* geneseqp2000s:\* geneseqp2001s:\*

The present sequence is derived from a human MAGE-A1 HLA (human leukocyte antigen) class II-binding protein. Peptides derived from the MAGE-A1 HLA binding protein stimulate the activity and proliferation of CD4+ T lymphocytes. The MAGE-A1 HLA binding protein is useful as a diagnostic agent for diagnosing a disorder characterized by expression of MAGE-A1. The protein is used for treating a disorder characterized by expression of MAGE-A1 such as cancers e.g. melanomal, squamous cell carcinomas, colorectal carcinomas, osteosarcomas, and lymphocytic leukemias. Peptides derived from the MAGE-A1 HLA binding protein are useful in the production of anti-tumour vaccines Novel MAGE-A1 human leukocyte antigen class II peptides which bind to and are presented to the class II molecules, useful for inducing immune response and treating cancers characterized by expression of MAGE-A1. Van Der Bruggen P; MAGE-A1, HLA, human leukocyte antigen; CD4+ T lymphocyte; cancer; MAGE-A1 HLA class II-binding protein; vaccine. Peptide derived from human MAGE-Al HLA class II-binding protein. Boon-Falleur T, Ė Chaux P, Claim 3; Page 43; 78pp; English. AAB31295 standard; peptide; 12 (LUDW-) LUDWIG INST CANCER RES. 14-JUN-2000; 2000WO-US016287. 99US-00336091. (first entry) Van Snick J, Lethe B, WPI; 2001-102698/11. WO200078806-A1. Homo sapiens. 18-JUN-1999; 20-APR-2001 28-DEC-2000. AAB31295; 

Sequence 12 AA;

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WO200190197-A1
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                                                                    Homo sapiens
                                                                                                                                                       18-JUN-1999;
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lymphocytes. The MAGE-A1 HLA binding protein is useful as a diagnostic agent for diagnosing a disorder characterized by expression of MAGE-A1. The protein is used for treating a disorder characterized by expression of MAGE-A1 such as cancers e.g. melanomal, squamous cell carcinomas, of MAGE-A1 such as sosteedsarcomas, and lymphocytic leukemias. Peptides derived from the MAGE-A1 HLA binding protein are useful in the production
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  Score 57; DB 4; Length 12;
Pred. No. 0.0001;
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ive 0; Mismatches 0;
                                                                                                                       AAB31291 standard; peptide; 16 AA.
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Matches 12; Conservative
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Matches 12; Conserv
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The present sequence is derived from a human MAGE-A1 HLA (human leukocyte antigan) class II-binding protein. Peptides derived from the MAGE-A1 HLA binding protein stimulate the activity and proliferation of CD4+ T lymphocytes. The MAGE-A1 HLA binding protein is useful as a diagnostic agent for diagnosing a disorder characterized by expression of MAGE-A1. The protein is used for treating a disorder characterized by expression of MAGE-A1 cotoin as cancers e.g. melanomal, squamous cell carcinomas, octooaxarcomas, and lymphocytic leukemias. Peptides derived from the MAGE-A1 HLA binding protein are useful in the production
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                                                      MAGE-A1; HLA; human leukocyte antigen; CD4+ T lymphocyte; cancer;
MAGE-A1 HLA class II-binding protein; vaccine.
Peptide derived from human MAGE-Al HLA class II-binding protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Boon-Falleur T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Preu...ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chaux P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; Page 42; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                          14-JUN-2000; 2000WO-US016287.
                                                                                                                                                                                                                                                                                                                                                                                                                               99US-00336091.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of anti-tumour vaccines
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AAQ85435 encodes AAR70909 human melanoma antigen MAGE-1, it was used to produce the C-terminal MAGE-1 peptides described in AAR70915 to AAR70969.
These peptides are useful for defining epitopes that engender a HLA-restricted cytotoxic lymphocyte activity against MAGE-1 antigens. Compans. containing these peptides can be administered, as a vaccine to patients susceptable to MAGE associated tumours, e.g. melanomas. (Updated on 25-MAR-2003 to correct PV field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This is the amino acid sequence of human tumour rejection antigen precursor (TRAP) MAGE-A1. MAGE-A1 cDNA (see AAV69719) shows homology to novel human MAGE-C1 cDNA (see AAV69720). MAGE-C1 (see AAW81546) is a novel member of the MAGE family that may be recognised by cytotoxic Tells, leading to lysis of the tumour cells which express it. It is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumour rejection antigen precursors – used for determining presence of cytolytic T cells specific for complexes of a human leukocyte antigen.
                                                                                                                                                                                                       Human melanoma antigen, MAGE-1, peptide(s) - useful for stimulating immune response against melanoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAGE-Al; human; tumour rejection antigen precursor; TRAP; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 57; DB 2; Length 309; 100.0%; Pred. No. 0.0039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                              Sidney JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumour rejection antigen precursor MAGE-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 50-51; 84pp; English.
                                                                                           Sette AD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Boon-Falleur T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW81548 standard; protein; 309 AA.
                                                                                                                                                                                                                                                                     Example 1; Fig 1; 59pp; English.
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    93US-00103623
                                                                                           BD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12; Conservative
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                                                                                         Livingston
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                                                                                                                                       WPI; 1995-090681/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-024041/02
                                                (CYTE-) CYTEL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAV69719
                                                                                                                                                         N-PSDB; AAQ85435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 309 AA;
    06-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9849184-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnosis.
                                                                                           Fikes JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lucas S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW81548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW81548
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                                                                                                                                                                                                                                                                                                                                              The invention relates to a new synthetic polypeptide (I) comprising several different segments of at least one parent polypeptide linked together in a different relationship relative to their linksed in the parent polypeptide to imped, abrogate or otherwise alter at least one function associated with the parent polypeptide and for inducing an immune response against a pathogen or cancer. Also included are a synthetic polypeptides. The synthetic polypeptides and a computer system for designing the synthetic polypeptides. The synthetic polypeptides and polymucleotides or are referred to as a Savine. The synthetic polypeptide is useful for modulating immune responses preferably directed against a pathogen or a cancer, (e.g., cancers of the lung, breat, ovary, cervix, colon, head and neck, pancreas, prostate, stomach, bladder, kidney, bone liver, cospophagus, brain, testicle, uterus), as potentiating agents.

Compositions comprising the polypeptide may be used in the treatment or prophylaxis against virus (such as infections caused by HIV (human immunodeficiency virus), hepstitis, influenza, Japanese encephalitis virus, Epstein-Barr virus and respiratory syncytial virus), bacterial (e.g., infections caused by Neisseria, Meningococcal, Haemophilus, C. (e.g., infections caused by Plasmodium, Schistosoma, Leishmania, Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                New synthetic polypeptides having several different segments of at least one parent polypeptide linked together differently compared to the linkage in the parent polypeptide, for inducing immune response against a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 57; DB 5; Length 30; 100.0%; Pred. No. 0.00029;
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                                                                                                                                                                                                                                                                                                            Example 3; Fig 27; 364pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human melanoma antigen MAGE-1.
26-MAY-2000; 2000AU-00007761.
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                                           (AUSU ) UNIV AUSTRALIAN NAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (revised)
                                                                                                                                  WPI; 2002-147575/19.
                                                                                                                                                                                                                                                                     pathogen or cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 12; Conserv
                                                                                                                                                       N-PSDB; ABK36862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 30 AA;
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09-OCT-1995
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Gaps

(first entry)

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AAE06806 standard; protein; 309 AA.
                                                                                                                                                                          Human MAGE-Al protein.
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                                                                                                          AAE06806;
                                      RESULT 8
AAE06806
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents a human MAGE-A1 HLA (human leukocyte antigen) class II-binding protein. Peptides derived from the MAGE-A1 HLA binding protein atimulate the activity and proliferation of CD4+ T lymphocytes. The MAGE-A1 HLA binding protein is useful as a diagnostic agent for diagnosing a disorder characterized by expression of MAGE-A1. The protein is used for treating a disorder characterized by expression of MAGE-A1 such as cancers e.g. melanomal, squamous cell carcinomas, colorectal carcinomas, osteosarcomas, and lymphocytic leukemias. Peptides derived from the MAGE-A1 HLA binding protein are useful in the production of anti-tumour vaccines
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expressed in a variety of tumours and in normal testis cells, but not by other normal cells. The invention provides MACE-C1 and MACE-C2 nucleic acids and polypeptides, useful e.g. in a claimed method for determining the presence of cytolytic T cells specific for complexes of a human leukocyte antigen (HLA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel MAGE-A1 human leukocyte antigen class II peptides which bind to are presented to the class II molecules, useful for inducing immune response and treating cancers characterized by expression of MAGE-A1.
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                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid sequence of human MAGE-Al HLA class II-binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAGE-A1; HLA; human leukocyte antigen; CD4+ T lymphocyte; cancer; MAGE-A1 HLA class II-binding protein; vaccine.
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                                                                                                                                      100.0%; Score 57; DB 2; Length 309, 100.0%; Pred. No. 0.0039;
                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chaux P, Boon-Falleur T,
                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                             AAB31290 standard; protein; 309 AA.
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                                                                                                                                                                                                                             281 EYVIKVSARVRF 292
                                                                                                                                                      Local Similarity 100.
1es 12; Conservative
                                                                                                                                                                                                          1 EYVIKVSARVRF 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-102698/11.
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                                                                                                      Sequence 309 AA;
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                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Functional variants and isolated mimetics of a MAGE-Al HLA-B35 or HLA-B44 binding peptide, used in diagnosis and treatment of a disorder characterized by expression of MAGE
MAGE antigenic peptide; Human leukocyte antigen; HLA-B35; HLA-B44; tumour cell; immunostimulant; antigen presentation; cancer; melanoma; CD8+ cytotoxic T lymphocyte; colorectal; prostate; gastric carcinoma; myeloma; brain tumour; sarcoma; seminoma; ovarian tumour; cytostatic; gene therapy; human; MAGE-A1; tumour rejection antigen; TRA.
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100.0%; Pred. No. 0.0039;
ive 0; Mismatches 0; Indels
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Schultz E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Page 86-87; 103pp; English.
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25-OCT-2000; 2000US-0243212P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-488724/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                            WO200153833-A1.
                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                      26-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Luiten R,
Demotte N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -A1 or -A3
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RESULT 9 AAU84814

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Gaps

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100.0%; Score 57; DB 4; Length 309; 100.0%; Pred. No. 0.0039; Pred. 0; Mismatches 0; Indels

Conservative 1 EYVIKVSARVRF 12

Best Local Similarity Matches 12; Conserv

ò

Query Match

281 EYVIKVSARVRF 292

Human, epitope, vaccine, immunotherapeutic; cytostatic; immunogenicity; I cell.

Human MAGE-1 protein SEQ ID.NO:71.

(first entry)

03-FEB-2003

ABP74195;

ABP74195 standard; protein; 309 AA.

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The invention relates to a new synthetic polypeptide (I) comprising several different segments of at least one parent polypeptide linked together in a different relationship relative to their linked elements of a different relationship relative to their linked in the parent polypeptide and in the parent polypeptide and for inducing an immune response against a pathogen or cancer. Also included are a synthetic polypeptides. The synthetic polypeptides and polymotleotides or synthetic polypeptides. The synthetic polypeptides and polymotleotides or are referred to as a Savine. The synthetic polypeptide is useful for modulating immune responses preferably directed against a pathogen or a cancer, (e.g., cancers of the lung, breat, ovary, cervix, colon, head and neck, pancreas, prostate, stomach, bladder, kidney, bone liver, cospopagus, brain, testicle, uterus), as potentiating agents.

Compositions comprising the polypeptide may be used in the treatment or prophylaxis against virus and respiratory and respiratory syncytial virus), bacterial (e.g., infections caused by Neisseria, Meningococcal, Haemophilus, cvirus, Epstein-Barr virus and respiratory syncytial virus), bacterial (e.g., infections caused by Plasmodium, Schistosoma, Leishmania, Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is comparion.
                                                                                                                                                                                                                                                                                                                                                                                       New synthetic polypeptides having several different segments of at least one parent polypeptide linked together differently compared to the linkage in the parent polypeptide, for inducing immune response against a
                                                                                                      Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus; viral infection; human immunodeficieny virus; melanoma; bacterial infection; Salmonella; Legionella; parasitic infection; Trypanosoma; Toxoplasma; Giardia.
AAU84814 standard; protein; 309 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; Fig 27; 364pp; English.
                                                                            Human MAGE-1 consensus sequence.
                                                                                                                                                                                                                                                    25-MAY-2001; 2001WO-AU000622.
                                                                                                                                                                                                                                                                               26-MAY-2000; 2000AU-00007761.
                                                                                                                                                                                                                                                                                                         (AUSU ) UNIV AUSTRALIAN NAT.
                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                   Thomson SA, Ramshaw IA;
                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-147575/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                pathogen or cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 309 AA;
                                                                                                                                                                                                 WO200190197-A1.
                                                                                                                                                                        Homo sapiens.
                                                    08-MAY-2002
                                                                                                                                                                                                                            29-NOV-2001
                        AAU84814;
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Novel epitopes useful as vaccines, comprises peptides or nucleic acid encoding the peptides, that are useful epitopes of target-associated

Claim 1; Page 156; 352pp; English.

antigens.

Xie Z;

Liu L,

Simard JJL, Diamond DC,

WPI; 2003-067518/06. N-PSDB; AB083847

(CTLI-) CTL IMMUNOTHERAPIES CORP

06-APR-2001; 2001US-0282211P. 07-NOV-2001; 2001US-0337017P.

04-APR-2002; 2002WO-US011101.

WO200281646-A2. Homo sapiens.

17-0CT-2002

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The present invention describes an isolated epitope (I) and an epitope cluster. Also described is a vaccine or immunotherapeutic composition (VC) comprising (I). (I) has cytostatic activity. VC is useful for treating an animal, by administraing to an animal the vaccine or immunotherapeutic composition. VC is also useful for evaluating immunotherapeutic composition. VC is also useful for evaluating composition. VC is also useful for evaluating immunogenicity of a vaccine or immunotherapeutic composition, by administering VC to an HLA-transgenic animal and evaluating immunogenicity based on a characteristic of the animal, or by in vitro immunogenicity based on a characteristic of the animal, or by in vitro primary stimulation of a T cell and evaluating immunogenicity. (I) is useful for determining specific T cell frequency, by contacting T cells with a MHC-peptide complex, and further comprises ELISPOT analysis, limiting dilution analysis, flow cytometry, in situ hybridisation and/or polymerase chain reaction (PCR). ABQ83843 to ABQ83858 and ABP74128 to ABP74131 represent sequences used in the exemplification of the present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 57; DB 6; Length 309; 100.0%; Pred. No. 0.0039; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human tumour rejection antigen precursor, MAGE-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABU08930 standard; protein; 309 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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281 EYVIKVSARVRF 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
hes 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EYVIKVSARVRF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 309 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABU08930;
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Gaps

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cch 100.0%; Score 57; DB 5; Length 309; sl Similarity 100.0%; Pred. No. 0.0039; 12; Conservative 0; Mismatches 0; Indels

Best Local Similarity Matches 12, Conserv

Query Match

1 EYVIKVSARVRF 12

ð සු RESULT 10 ABP74195

Xie Z;

Liu L,

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Epitope having high affinity for major histocompatibility complex class I useful for treating an animal, evaluating immunogenicity of a vaccine or therapeutic composition and for diagnosing a disease.
                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 71; 239pp; English
                                                                                                                                                                                                    (CTLI-) CTL IMMUNOTHERAPIES CORP.
                                                                                                                                           06-APR-2001; 2001US-0282211P.
07-NOV-2001; 2001US-0337017P.
07-MAR-2002; 2002US-0363210P.
                                                                                                                29-MAR-2002; 2002WO-US010189.
                                                                                                                                                                                                                                Simard JJL, Diamond DC,
                                                                                                                                                                                                                                                            WPI; 2003-248010/24.
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                                                           WO2003008537-A2
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    immuni sation.
                                Unidentified.
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                                                                                       30-JAN-2003.
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    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid molecule which encodes a tumour rejection antigen precursor (TRAP) having an amino acid sequence of a tumour rejection antigen precursor (TRAP) having an amino acid sequence of a TRAP encoded by a fully defined MAGE-G3, MAGE-B6, or MAGE-B6 polynuclectide sequence. Also disclosed is a method which is useful for determining presence of cytolytic T-cells specific for complexes of human cleukoryte antigen (HLM) and a peptide derived from the nucleic acid in a cytocoxic T-lymphocyte (CTL)-containing sample. The nucleic acid is useful as a diagnostic probe to determine the presence of abnormal cumour) cells such as seminoma, bladder transitional-cell carcinoma, head-and-neck squamous-cell carcinoma, breast carcinoma, sarcoma, cutaneous melanoma or nonsmall cell lung cancer (NSCLC) which express MAGE-G1, MAGE-B5 or MAGE-B6. The nucleic acid is useful for diagnosing a disorder characterised by expression of MAGE-C1, MAGE-B5 or MAGE-B6 TRAPS or tumour rejection antigens (TRAP). The present sequence represents the amino acid sequence of the human tumour rejection antigen precursor, MAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
TRAP; tumour rejection antigen precursor; cytolytic T-cell; CTL; tumour; seminoma; bladder transitional-cell carcinoma; NSCLC; adaptor; head-and-neck squamous-cell carcinoma; breast carcinoma; sarcoma; cutaneous melanoma; nonsmall cell lung cancer; MAGE-A1; human.
                                                                                                                                                                                                                                                                                                                                                                        Novel isolated nucleic acid encoding tumor rejection antigen precursor MAGE-C3, MAGE-B5, or MAGE-B6, useful as diagnostic probes to determine presence of abnormal e.g., tumor cells expressing MAGE-C1, MAGE-B5 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Epitope; immunological; vaccine; major histocompatibility complex class I; MHC class I; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 57; DB 6; Length 309; 100.0%; Pred. No. 0.0039; live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADC09573 standard; protein; 309 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 2; 59pp; English.
                                                                                                                                                                                    97US-00845528.
98US-00066281.
99US-00468433.
                                                                                                                                                           01-MAR-2002; 2002US-00085108.
                                                                                                                                                                                                 24-APR-1998; 98US-00066281
17-DEC-1999; 99US-00468433
09-FEB-2000; 2000US-00501104
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                                                                                                                                                                                                                                                                                                    Boon-Falleur T;
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                                                                                                                                                                                                                                                           LUCAS S.
BOON-FALLEUR T.
                                                                                                                                                                                                                                                                                                                                WPI; 2003-328468/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
les 12; Conserv
                                                                                                                                                                                                                                                                                                                                              N-PSDB; ABX93696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 309 AA;
                                                                                                   US2002176865-A1
                                                                                                                                                                                  25-APR-1997;
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                                                                                                                             28-NOV-2002
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                                                                                                                                                                                                                                                                                                    Lucas S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                         (LUCA/)
                                                                                                                                                                                                                                                                                                                                                                                                                     MAGE-B6
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The invention relates to an isolated epitope polypeptide that has high affinity for major histocompatibility complex (MHC) class I, and an epitope cluster comprising the polypeptide. Also disclosed is a vaccine or immunotherapeutic composition containing an epitope of the invention. Compositions of the invention may be used in the treatment of cancer. The method can be combined with a radiation therapy, themotherapy, the corposition is also useful for evaluating immunogenicity of a vaccine or immunotherapeutic compound. Multimeric MHC repptide complexes of the invention are useful for determining specific T cell frequency. This method is useful for evaluating immunological invention step compositions to and subsequent to an diagnosition are useful for diagnosity and alsease. The current sequence represents an epitope of the invention are useful for invention with high affinity for MHC class I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stabilised mRNA, translation optimised, vaccine, tissue repair; sequence modification determination; gene therapy; cytostatic; virucide, antibacterial; protozoacide, nootropic, neuroprotective; infection; antiparkinsonian; immunostimulant; cancer; MAGEI protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA019742 standard; protein; 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-AUG-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wild-type MAGE1 protein.
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The invention describes a purified polypeptide, which comprises a fragment of a kinase, phosphatase, protease, protease inhibitor, transporter, cytoskeletal protein, receptor or transcription factor. The polypeptide is useful as an immunogenic composition for eliciting in a mammal an immunogenic response directed against any of the purified polypeptide. The purified polypeptide, or the antibody that binds to this polypeptide, is useful for treating cancer. The polypeptide is also useful for identifying compounds that binds to a naturally processed class I or class II MHC-binding polypeptide. The polypeptides and particularly useful for treating or preventing myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, lymphoma or leukaemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an treating the above mentioned diseases. This sequence represents an profiling. Note: This sequence does not appear in the printed profiling appearing the above mentioned diseases on appear in the printed profile profile the profile of the polypeptide in electronic format directly from WIPO at
                                                                   New polypeptides (e.g. kinases, phosphatases, proteases, transporters, cytoskeletal proteins, receptors or transcription factors), useful for treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAGE-1; CLYTA-MAGE-1-His; fusion protein; tumour; melanoma;
breast cancer; bladder cancer; lung cancer; colon cancer;
head and squamous cell carcinoma; oesophagus carcinoma; vaccine; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gape
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                                                                                                                                                                                        Example 2; SEQ ID NO 1085; 134pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY06592 standard; protein; 445 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-EP000660.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 288 EYVIKVSARVRF 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
12; Conserve
                          WPI; 2003-040607/03.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 316 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
Synthetic.
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    ö
                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to a pharmaceutical composition containing at least one modified RNA encoding a biologically active or antigenic protein. The RNA is modified to optimise translation of the sequence. The compositions are used for vaccination against a wide range of infectious diseases (viral, bacterial or protozoal) or cancer, or for tissue regeneration, e.g. in cases of Alzheimer's or Parkinson's diseases and arthritis, but also to express proteins such as dystrophins, chloride ion channels (for treating cystic fibrosis) and enzymes (either for treating metabolic disorders or for synthesis of neurotransmitters such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Translational profiling; expressed protein tag; EPT; kinase; phosphatase; protease; protease inhibitor; transporter; cytoskeletal protein; receptor; transcription factor; cancer; MHC; major histocompatability complex; myeloma; colon cancer; gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                    Composition containing mRNA modified for optimal translation and stability, useful for treating e.g. tumors or infections, comprises increased G/C content and fewer rare codons.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dopamine). The present sequence is the wild-type MAGE1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 57; DB 6; Length 310; 100.0%; Pred. No. 0.0039; Pred. 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human expressed protein tag (EPT) #1085.
                                                                                                                                       Pascolo S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chicz RM, Tomlinson AJ, Urban RG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABU04419 standard; protein; 316 AA.
                                                                                                                                                                                                                                                                                                                                                 Disclosure, Fig 2B; 75pp; German.
05-JUN-2002; 2002WO-EP006180.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-MAY-2001; 2001US-0292544P.
08-AUG-2001; 2001US-0310801P.
01-OCT-2001; 2001US-033670P.
20-PEB-2002; 2002US-0358985P.
                                           05-JUN-2001; 2001DE-01027283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-MAR-2002; 2002WO-US009671.
                                                                                                                                       Von Der Muelbe F, Hoerr I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-JAN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EYVIKVSARVRF 291
                                                                                         (VMUE/) VON DER MUELBE F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12; Conservative
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                                                                                                                                                                                 WPI; 2003-148621/14.
N-PSDB; ABZ69107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 310 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200278524-A2
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New protein derivatives used in cancer vaccine therapy for treating a range of cancers including melanomas, carcinomas and cancers of breast.
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Example 9; Page 69-70; 72pp; English.

The present sequence represents a fusion protein composed of the C-terminal portion of the Streptococcus pneumoniae LYTA protein (CLYTA), the human MAGE-1 tumour-associated antigen and a hexahistidine tail. A vector designed for recombinant expression of the fusion protein in Bscherichia coli is provided. The CLYTA moiety provides expression of soluble fusion protein, facilitates affinity purification, and also acts as a T-helper epitope. The invantion relates to MAGE proteins fused to an immunological fusion partner, e.g. CLYTA-MAGE-I-His. These novel fusion proteins provide vaccines for immunotherapy of melanomas or other MAGE-associated tumours like breast, bladder, lung and non-small cell lung cancer, head and squamous cell carcinoma, colon carcinoma and oesophagus carcinoma 

Sequence 445 AA;

0; Gaps 100.0%; Score 57; DB 2; Length 445; 100.0%; Pred. No. 0.0059; Live 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.
Matches 12; Conservative

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1 EYVIKVSARVRF 12 à ద Search completed: October 7, 2004, 15:13:03 Job time : 48.1818 secs

Appli, Apply Apply

Sequence Sequence Sequence

Sequence Sequence Sequence Sequence

Sequence Sequence Sequence Sequence

Sequence

OM protein

Run on:

Sequence:

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Sequence 1, Application US/08465167A; Patent No. 5780395; GENERAL INFORMATION:
APPLICANT: Fikes, John D.
APPLICANT: Sette, Alessandro D.
APPLICANT: Sidney, John C.
TITLE OF INVENTION: IMMUNOGENIC PEPTIDES (as amended); TITLE OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP.
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 57; DB 1; Length 58; ilarity 100.0%; Pred. No. 0.00042; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAPPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,167A
FILING DATE: 05-JUN-1995
CLASSIFICATION NUMBER: US 08/103,623
FILING DATE: 06-JUN-1995
ATORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 39
ATORNEY/AGENT INFORMATION:
NAME: PATMELE, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-60-1
TELEPHONE: 120-467-9600
US-09-107-532A-6086
US-09-222-991A-2975
US-09-222-991A-27118
US-09-222-991A-27115
US-09-107-532A-477
US-09-107-532A-477
US-09-107-532A-477
US-08-96-16-170
US-08-906-16-170
US-08-906-613-170
US-09-012-431-170
US-08-906-613-170
US-08-906-613-170
US-08-906-613-170
US-08-906-613-170
US-08-906-613-170
US-08-906-613-172
US-08-906-414-172
US-08-906-414-172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALUNESSEE: Townsend and Townsend and Crew STREET: Two Embarcadero Center, 8th Floor STATE: CA
                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: US
ZIP: 98111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-465-167A-1
                                                                                                                                                                                                                                                                                                                                                                                 US-08-465-167A-1
    5371, Ap
33, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                           ; Search time 13.0909 Seconds (without alignments) 47.324 Million cell updates/sec
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Sequence 10
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Sequence 1
Sequence 5
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(/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

(/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

(/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

(/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

(/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

(/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

(/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-465-167A-1
US-08-627-820-1
US-08-465-167A-24
US-08-93-118-10
US-08-845-528C-10
US-08-62-281B-10
US-09-392-114-29
US-09-392-114-29
US-08-159-339A-595
US-08-159-339A-595
US-08-159-139A-595
US-08-65-167A-15
US-08-465-167A-8
US-08-465-167A-8
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US-08-65-167A-8
US-08-65-167A-8
US-08-65-167A-8
US-08-65-167A-8
US-08-65-167A-331
US-08-65-167A-331
US-08-65-167A-331
US-08-65-167A-331
US-08-65-167A-331
US-08-65-167A-331
US-08-65-167A-331
US-08-465-167A-38
                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                  389414 segs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                           October 7, 2004, 15:18:26;
                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                             - protein search, using sw model
                                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                              seq length: 0
seq length: 200000000
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57
1 EYVIKVSARVRF 12
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Match Length
                                                                                                                                                                                                                                      Scoring table:
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Minimum DB 8 Maximum DB 8

Database

Result

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Gaps

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Sequence 10, Application US/08993118
Patent No. 5997872
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
BOON-PALIEUR, THIERY
TITLE OF INVENTION:
FEJECTION ANTIGEN PRECURSOR MAGE-C1 AND USES
TITLE OF INVENTION:
THEREOF INVENTION:
THEREOF INVENTION:
THEREOF INVENTION:
THEREOF INVENTION:
THEREOF INVENTION:
THEREOF THEREOF
NUMBER OF SEQUENCES:
14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 57; DB 1; Length 309; 100.0%; Pred. No. 0.0026; Pred. No. 0. 100.0%; ive 0; Mismatches 0; Indels
TITLE OF INVENTION: IMMUNOGENIC PEPTIDES (as amended)
NUMBER OF SEQUENCES: 5.
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Riopy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Riopy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,167A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
FRICK APPLICATION ADATA:
APPLICATION NUMBER: US 08/103,623
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: PATMELE, STEVEN W.
REGISTRATION NUMBER: 31,990
REGISTRATION NUMBER: 14137-60-1
TELEPHONE: 206-467-9600
TELEFRACE AFFERENCE/DOCKET NUMBER: 14137-60-1
TELEFRONE: 215-576-0300
TELEFRACE CHARACTERISTICS:
LEMETHE TO SEQUENCE CHARACTERISTICS:
LEMETHE TO SECUENCE CHARACTERISTICS:
LEMETHE TO S
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: 1BM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,118
FILING DATE:
                                                                                                                         Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Felfe & Lynch
805 Third Avenue
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amino acid
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Best Local Similarity luv...
12, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: New York City
STATE: New York
COUNTRY: USA
                                                                                                                            STREET: Two Embarcad
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-465-167A-24
                                                                                                                                                                                  STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 4
US-08-993-118-10
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0
                                                                                                                                                                                                                                                                                                                              APPLICANT: Fikes, John D.
Livingston, Brian D.
Sette, Alessandro D.
Sidney, John C.
TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTY: U.S.A.

SIALE: 94105

COMPUTER READBLE FORM:

MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACHILIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627, 820
FILING DATE: 02-Apr-1996
CLASSIFICATION: <URNown>
PRIOR APPLICATION NUMBER: US/08/103, 623
ATYORNEY/AGENT INFORMATION:
NAME: PATHORNEY/AGENT INFORMATION:
NAME: PATHORNEY AGENT INFORMATION:
TELEPHONE: (206) 467-9600
TELEPHONE: (206) 467-9600
TELEPAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 58;
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US-08-465-167A-24

Sequence 24, Application US/08465167A

Patent No. 5750395

GENERAL INFORMATION:
APPLICANT: Livingston, Brian D.
APPLICANT: Livingston, Brian D.
APPLICANT: Sette, Alessandro D.
APPLICANT: Sidney, John C.
TITLE OF INVENTION: DNA ENCODING MAGE-1 C-TERMINAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 57; DB 4; L6
100.0%; Pred. No. 0.00042;
Mismatches 0;
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                                                                                                                                                                                                                                        Sequence 1, Application US/08627820 Patent No. 6464980 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 58 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 100.
Matches 12; Conservative
                               EYVIKVSARVRF 12
                                                                  30 EYVIKVSARVRF 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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Gaps

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Sophie; DE SMET, Charles; BOON-FALLEUR, Thierry
: ISOLATED NUCLEIC ACID MOLECULE CODING
: FOR TUMOR REJECTION ANTIGEN PRECURSOR MAGE-C1 AND MAGE-C2
: AND USES THERED
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                                                                                                                                                                                                                                                        APPLICANT: Fikes, John D.
Livingston, Brian D.
Sette, Alessandro D.
Sidney, John C.
Sidney, John C.
TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 57; DB 4; Length 309; 100.0%; Pred. No. 0.0026; Pred. No. 0.0026; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               STREET: One Market Plaza, Steuart Street Tower STREET: One Market Plaza, Steuart Street Tower Strarp.
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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  Mismatches
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ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-60
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/627,820
FILING DATE: 02-Apr-1996
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/103,623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-08-627-820-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (206) 467-9600
                                                                                                                                                                                           Sequence 24, Application US/08627820 Patent No. 6464980 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            543-5043
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (415) 543-5
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
                                                                    281 EYVIKVSARVRF 292
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Best Local Similarity 100.
Matches 12; Conservative
  12; Conservative
                                           1 EYVIKVSARVRF 12
                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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  Matches
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APPLICANT: DE SMET, Charles;
APPLICANT: DE SMET, Charles;
APPLICANT: DE SMET, Thierry
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE CODING FOR TUMOR
TITLE OF INVENTION: REJECTION ANTIGEN PRECURSOR MAGE-C1 AND USES
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 57; DB 2; Length 309; Best Local Similarity 100.0%; Pred. No. 0.0026; Matches 12; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPLOY EXECUTE STEM FS/2 CONTROL SYSTEM: PC-DOS SOFTWARE: Wordperfect CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/845,528C FILING DATE: April 25, 1997 CLASSIFICATION: 4333 ATTORNEY/AGENT INFORMATION: NAME: MARY ANNE SCHOÉIGLÉ REGISTATION NUMBER: 36,669 REPERBUCE/DOCKET NUMBER: LUD 5455 TELECOMMUNICATION: INFORMATION:
           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/845,528
FILING DATE: APATI 25, 1997
ATTORNEY/AGENT INFORMATION:
NAME: MARY ANNE Schoffeld
REGISTRATION NUMBER: 15,669
REFERENCE/DOCKET NUMBER: LUD 5455
TELECOMMUNICATION INFORMATION:
TELECHONE: (212) 688-9200
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 838-3884
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10, Application US/08845528C Patent No. 6027924 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                               ; TYPE: amino acids
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
US-08-993-118-10
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ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (212) 688-9200
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EYVIKVSARVRF 12
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Best Local Similarity
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US-09-392-714-29
US-09-392-714-29
Sequence 29, Application US/09392714A
Patent No. 6686147
GENERAL INFORMATION:
APPLICANT: Gure, All O.
APPLICANT: Williamson, Barbara
APPLICANT: WINVENTON: Therefor
FILE REFERENCE: L0461/7062
CURRENT APPLICATION NUMBER: PCT/US98/14679
EARLIER FILING DATE: 1998-07-15
MUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 29
LENGTH: 309
LTYPE: PDT
TYPE: PDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
US-08-465-167A-15
; Sequence 15. Application US/08465167A
; Patent No. 5750395
; GENERAL INFORMATION:
; APPLICANT: Fikes, John D.
; APPLICANT: Gette, Alessandro D.
; APPLICANT: Sidney, John C.
; TITLE OF INVENTION: DNA ENCODING MAGE-1 C-TERMINAL
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES (as amended)
; NUMBER OF SEQUENCES: 51
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/845,528
FILING DATE: April 25, 1997
ATTORNEY/AGENT INFORMATION:
NAME: MARY ANNE SCHOFİƏLİ
REGISTRATION NUMBER: 15,669
REFERENCE/DOCKET NUMBER: LUD 5611 JEL/MAS
TELEPHONE: (202) 662-0200
TELEPHONE: (202) 662-0200
TELEPRA: (202) 662-4643
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                               ; TYPE: amino acids
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
US-09-468-433C-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           281 EYVIKVSARVRF 292
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Best Local Similarity 100.
Matches 12; Conservative
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Matches 12; Conservative
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US-09-392-714-29
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; Sequence 10, Application US/09468433C
; Patent No. 6680191
; GENERAL INFORMATION:
; APPLICANT: LUCAS, Sophie; BOON-FALLEUR, Thierry
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES CODING FOR
; TITLE OF INVENTION: MAGE-B FAMILIES AND USES THEREOF
; TITLE OF INVENTION: MAGE-B FAMILIES AND USES THEREOF
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; CITY: Washington
; STREET: District of Columbia
; CUNTY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                       COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM PSYZ
OPERATING SYSTEM:
PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/066,281B
FILING DATE: April 24, 1998
CLASSIFICATION NUMBER: US/845,528
FILING DATE: April 25, 1997
ATTORA PEPLICATION NUMBER: 08/845,528
FILING DATE: April 25, 1997
ATTORA SEPERATION NUMBER: 36,669
REFERENCE/DOCKET NUMBER: 36,669
REFERENCE/DOCKET NUMBER: 36,669
REFERENCE/DOCKET NUMBER: 36,669
REFERENCE/CLASTON NUMBER: 36,669
REFERENCE/CLASTON NUMBER: 36,669
REFERENCE/CLASTON NUMBER: 1200
TELLECOMMUNICATION INFORMATION:
TELEPRAN: (212) 318-3100
TELEFAX: (212) 325-5596
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 2004
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordberfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/468,433C
FILING DATE: December 17, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                              ADDRESSEE: Fulbright & Jaworski L.L.P. STREET: 666 Fifth Avenue CITY: New York City STATE: New York COUNTRY: USA ZIP: 10103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acids
STRANDEDNESS: single stranded
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: 09/066,
FILING DATE: April 24, 1998
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Best Local Similarity 100.
Matches 12; Conservative
  NUMBER OF SEQUENCES: 20
                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright
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Livingston, Brian D.
Sette, Alessandro D.
Sidney, John C.
TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Street Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 10;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 46; DB 3;
Pred. No. 0.0084;
                       FILING DATE: 07-AUG-1992
APPLICATION WINBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-005030US
TELECHOME: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/103,623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READELE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
    US 07/926,666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 02-Apr-1996
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (206) 467-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 15, Application US/08627820
Patent No. 6464980
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: <Unknown> ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 10 amino acide
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100.0%;
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                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SS
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Guery Match
Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A.
ZIP: 94105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 YVIKVSARVR 10
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      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-159-339A-595
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Fatent No. 6037135
GENERAL INFORMATION:
APPLICANT: Kubo, Ralph T.
APPLICANT: Grey, Howard M.
APPLICANT: Sette, Alessandro
APPLICANT: Carls, Esteban
TITLE OF INVENTION: Ubs
UMBER OF SEQUENCES: 1254
CORRESPONDENCES: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                     COMPUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,167A
FILING DATE: 05-UN-1995
CLASSIFICATION: DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/103,623
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: PARMEL-CAND NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-60-1
TELEPHONE: 206-467-9600
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARATICS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew Lip STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,339A
FILING DATE: 29-NOV-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 10 amino acids rYPE: amino acid
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Best Local Similarity 100.
Matches 10; Conservative
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US-08-465-167A-8
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Sequence 49, Application US/08465167A

Patent No. 5750395

GENERAL INFORMATION:

APPLICANT: Livingston, Brian D.

APPLICANT: Sette, John C.

TITLE OF INVENTION: DNA ENCODING MAGE-1 C-TERMINAL

TITLE OF INVENTION: IMMUNOGENIC PEPTIDES (as amended)

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: CA
                                                                                                                                                                                                                                                                               Query Match 80.7%; Score 46; DB 4; Length 10; Best Local Similarity 100.0%; Pred. No. 0.0084; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73.7%; Score 42; DB 1; Length 10; 100.0%; Pred. No. 0.05; tive 0; Mismatches 0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: PEDENTIAL
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 amino acids
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Best Local Similarity 100.
Matches 9; Conservative
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STRANDEDNESS: single
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MOLECULE TYPE: protein
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EYVIKVSAR 10
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RESULT 14

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Gaps
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US-08-465-167A-27

| Sequence 27, Application US/08465167A
| Patent No. 5750395
| GENERAL INFORMATION:
| APPLICANT: Fikes, John D. | APPLICANT: Sette, Alessandro D. | APPLICANT: State, John C. | TITLE OF INVENTION: DAPPLICANT: Staney, John C. | TITLE OF INVENTION: DAPPLICANT: Staney, John C. | TITLE OF INVENTION: DAPPLICANT: Staney, John C. | TITLE OF INVENTION: DATESS: | CORRESPONDENCE ADDRESS: | ADDRESSEE: Townsend and Townsend and Crew LLP | STREET: Two Embarcadero Center, 8th Floor | CITY: San Francisco
                                                           APPLICANT: Fires, John D.
APPLICANT: Fires, John D.
APPLICANT: Sette, Alessandro D.
APPLICANT: Sacte, Alessandro D.
APPLICANT: Sidney, John C.
TITLE OF INVENTION: INMUNOGENIC PEPTIDES (as amended)
NUMBER OF SEQUENCES:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                COUNTRY:

ZIP: 9811

ZIP: 9811

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BM PC COMPATION
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,167A
FILING DATE: 05-JUN-1995
FILING DATE: 07-77.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 41; DB 1;
Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 05-UNN-1995
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08 08/103,623
FILING DATE: 06-AUG-1993
ATYORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-60-1
Sequence 8, Application US/08465167A
Patent No. 5750395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71.9%; Sco
ilarity 100.0%; Pi
Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
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Best Local Similarity
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                                             GENERAL INFORMATION:
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COMPUTER READABLE FORM:

MEDIUM TYPE: PORPY disk

MEDIUM TYPE: TOPPY disk

COMPUTER: IBN PCOPY disk

COMPUTER: IBN PCOPY disk

MEDIUM TYPE: TOPS/MS-DOS

SOFTWARE: PARENTER PC-DOS/MS-DOS

SOFTWARE: PARENTER: W/08/465,167A

FILING DATE: 05-JUN-1995

FILING DATE: 05-JUN-1995

FILING DATE: 06-AUG-1993

ATYORNEY AGRYT INFORMATION:

NAME: PERMENCE DOCKET WINBER: 14137-60-1

FELECOMMUNICATION INFORMATION:

NAME: PERMENCE 106-67-9600

TELECOMMUNICATION INFORMATION:

NAME: PERMENCE 106-67-9600

TELECOMMUNICATION INFORMATION:

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TELECOMMUNICATION INFORMATION:

MARIE PERMENCE 106-67-9600

TELECOMMUNICATION INFORMATION:

MACHARCTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acids

TYPE: amino acids

TYPE: amino acids

TYPE: amino acids

TYPE: amino acids

TYPE: amino acids

TYPE: amino acids

TYPE: Amino acids

TYPE: Amino acids

TYPE: Amino acids

TYPE: Amino acids

TYPE: AMINO ACID:

MALCHIET PYPE: procein

US-08-465-167A-27

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MACHES 9; CONSETVATIVE 0; Mismatches 0; Indels 0; AND 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 INTENDENT 1 IN
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Search completed: October 7, 2004, 15:19:26 Job time : 14.0909 secs

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Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE
Sequence 33, Appl
Sequence 1278, Appl
Sequence 1278, Ap
Sequence 2, Appli
Sequence 10, Appl
Sequence 10, Appl
Sequence 11, Appl
Sequence 71, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                 October 7, 2004, 15:30:52; Search time 44.7273 Seconds (without alignments) 86.336 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                                                                                                                                                                                                                                                                                                                                                       Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_MEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/USO9E_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/USO9E_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/USO9E_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/USO08_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/USO08_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/USO08_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/USO08_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/USO08_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/USO08_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/USO08_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/USO08_PUBCOMB.pep:*
            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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S US-10-164-07BA-32
US-09-766-889A-2
US-09-766-889A-2
3 US-10-296-734-828
3 US-10-137-390-18
4 US-10-177-390-18
4 US-10-177-397-71
6 US-10-174-466-6
6 US-10-741-466-7
6 US-10-741-466-7
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8 US-10-741-466-7
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Maximum Match 100%
Listing first 45 summaries
                                                                       - protein search, using sw model
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seq length: 200000000
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1 EYVIKVSARVRF 12
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Sequence 33, Application US/10164121A
Sequence 33, Application World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World World Wor
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Sequence 274271,
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Sequence 11815, A
Sequence 66236, A
Sequence 68348, A
Sequence 168734,
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                                        4 US-10-128-711-93

4 US-10-128-711-93

5 US-10-149-138-4195

6 US-10-149-138-4195

6 US-10-149-138-4195

6 US-10-296-734-4145

5 US-10-296-734-1280

1 US-10-282-124-4145

6 US-10-117-937-128

2 US-10-218-025-2

2 US-10-218-025-2

2 US-10-218-025-2

2 US-10-218-025-2

6 US-10-282-122A-6049

6 US-10-78-191-19

6 US-10-78-191-19

7 US-10-282-122A-6049

1 US-01-298-453-11

2 US-10-243-55-530

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    ALIGNMENTS

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US-10-164-078A-32
Sequence 32, Application US/10164078A
Sequence 32, Application US/10164078A
Publication No. US20030228325A1
GENERAL INFORMATION:
APPLICANT: Blabbrough, Janine
APPLICANT: Schultz, Erwin
APPLICANT: Panichelli, Christophe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EYVIKVSARVRF 12
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1987
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ORGANISM: H. sapiens
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Matches 12; Conserv
US-10-164-121A-33
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Sequence 6, Appli Sequence 7, Appli Sequence 8, Appli Sequence 1454, Ap Sequence 129, App

Sequence 6 Sequence 7 Sequence 8 Sequence 1

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TUMOR REJECTION ANTIGEN PRECURSORS OF MEMBERS OF THE MAGE-C MAGE-B FAMILIES AND USES THEREOF
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Publication No. US20020176865A1
GENERAL INFORMATION:
APPLICANT: LUCAS, Sophie; BOON-FALLEUR, Thierry
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES CODING
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage COMPUTER: 1BM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Thompson, Scott A
APPLICANT: Thompson, Ian A
TITLE OF INVENTION: Synthetic molecules and uses therefor
FILE REFERENCE: Savine
CURRENT APPLICATION NUMBER: US/10/296,734
CURRENT FILING DATE: 2003-08-04
PRIOR APPLICATION UNDER: AU PQ7761/00
PRIOR FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 1507
SOFTWARE: PATENTIN version 3.2
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100.0%; Pred. No. 0.007;
ive 0; Mismatches 0;
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CORRESPONDENCE ADDRESS:
RADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: MAGE-1 consensus polypeptide US-10-296-734-828
                                                                                            PRIOR FILING DATE: 2000-10-25
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 828 Application US/10296734; Publication No. US20040054137A1; GENERAL INFORMATION:
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Best Local Similarity 100.
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ORGANISM: Artificial
                                                                                                                                                                                                                                                                                            Best Local Similarity
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US-10-296-734-828
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US-10-085-108-10
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LENGTH: 309
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RESULT 4
US-09-766-889A-2

US-09-766-889A-2

Sequence 2, Application US/09766889A

Patent No. US20020164654A1

GENERAL INFORMATION:
APPLICANT: Luten, Rosalie

APPLICANT: Scholar, Vincent
APPLICANT: Scholar, Vincent
APPLICANT: Scholar, Vincent
APPLICANT: Scholz, Erwin

APPLICANT: Scholz, Erwin

TILLE OF INVENTION: MAGE ANTIGENIC PEPTIDES WHICH BIND HLA-B44

FILLE REFERENCE: LO461/7104

CURRENT APPLICATION NUMBER: US/09/766,889A

CURRENT APPLICATION NUMBER: US 60/177,242

PRIOR FILING DATE: 2000-01-20

PRIOR APPLICATION NUMBER: US 60/243,212
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Sequence 1020405413741

Fublication No. US20040054137A1

GENERAL INFORMATION:

APPLICANT: Thompson, Scott A

APPLICANT: Rambhaw, Ian A

TITLE OF INVENTION: Synthetic molecules and uses therefor
FILE REFERENCE: Savine

CURRENT FILING DATE: 2003-08-04

FRIOR PILING DATE: 2003-08-04

PRIOR PLICATION NUMBER: AU PQ7761/00

PRIOR PLICATION NUMBER: 2000-05-26

NUMBER OF SEQ ID NOS: 1507

SOFTHARE: Patentin version 3.2

LENGTH: 30

LENGTH: 30
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100.0%; Score 57; DB 12; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 12; Conservative 0; Mismatches 0; Indels
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Pred. No. 0.00022;
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                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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US-10-296-734-1278
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Best Local Similarity 100.
Matches 12; Conservative
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FOR TUMOR REJECTION ANTIGEN PRECURSOR MAGE-C1 AND MAGE-C2 AND USES THEREOF
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  TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE CODING
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                                                                                                                                                                                                                                                         ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
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                                                                          NUMBER OF SEQUENCES: 20
CORRESSONDEMICE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 666 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/066,281B
FILING DATE: April 24, 1998
APPLICATION NUMBER: 08/845,528
FILING DATE: April 25, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/160,237
FLING DATE: 04-Jun-2002
CLASSIFICATION: «UNKNOWN»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: US 60/282,211
PRIOR PELING DATE: 2001-04-06
PRIOR PELING DATE: 2001-04-06
PRIOR PELING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: US 60/337,017
PRIOR PELING DATE: 2001-11-07
PRIOR FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 602
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 71, Application US/10117937
PUDICATION No. US20030220239A1
GENERAL INFORMATION:
APPLICANT: CTL IMMUNO THERAPIES CORP.
APPLICANT: SIMARD, John, J.L.
APPLICANT: DIAMOND, David, C.
APPLICANT: LIU, Liping
APPLICANT: LIU, Liping
APPLICANT: XIE, Zhidong
TITLE OF INVENTION: EPITOPE SEQUENCES
FILE REFERENCE: CTLIMM.027A
CURRENT FILING DAFE:
CURRENT FILING DAFE:
CURRENT FILING DAFE:
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US-10-160-237-10
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REGISTRATION NUMBER: 36,669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (212) 318-3100
                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (212) 752-5958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION
                                                                                                                                                                         CITY: New York City
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 10 SEQUENCE CHARACTERISTICS
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APPLICANT: Schuler, Gerold
APPLICANT: N.V. Antwerps Innovatiecentrum
TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
TITLE OF INVENTION: Polymucleotides by Electroporation
FILE REPERENCE: 021505wo/JH/ml
CURRENT APPLICATION NUMBER: US/10/177,390
CURRENT APPLICATION NUMBER: US/10/177,390
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-160-237-10
; Sequence 10, Application US/10160237
; Publication No. US20030170256A1
; GENERAL INFORMATION:
; APPLICANT: LUCAS, Sophie; DE SMET, Charles; BOON-FALLEUR, Thierry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                      NAME: Mary Anne Schoffeld
REGISTRATION NUMBER: 36,669
REFERENCE/DOCKET NUMBER: LUD 5611.1 JEL/MAS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3100
TELEFAX: (212) 318-3400
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/085,108
FILING DATE: 01-Mar-2002
CLASSIPICATION: <Unknown>
                                                                                                                    APPLICATION NUMBER: 09/501,104
FILING DATE: 09-Feb-2000
APPLICATION NUMBER: 09/468,433
FILING DATE: December 17, 1999
APPLICATION NUMBER: 09/066,281
FILING DATE: April 24, 1998
APPLICATION NUMBER: 08/845,528
FILING DATE: April 25, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acids
STRANDENESS: single stranded
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 18, Application US/10177390 Publication No. US20030143743A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                    PRIOR APPLICATION DATA:
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US-10-177-390-18
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LENGTH: 309
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; Sequence 1454, Application US/10296734
; Publication No. US20040054137A1
; GENERAL TRFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TILE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
                                                                                                                                 Sequence 7, Application US/10741466

Publication No. US20040180058A1

GENERAL INFORMATION:
APPLICANT: Sherman, M.
APPLICANT: Shneider, A.
TITLE OF INVENTION: Vaccine Compositions and Methods
FILE REFERENCE: 25955-003
CURRENT FILING DATE: 2003-12-19
PRIOR APPLICATION NUMBER: 60/435,500
PRIOR APPLICATION NUMBER: 60/435,500
PRIOR APPLICATION NUMBER: 60/435,500
SRIOR APPLICATION NUMBER: 60/435,500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 57; DB 16;
100.0%; Pred. No. 0.007;
ative 0; Mismatches 0;
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Publication No. US20040180058A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Influenza A virus
US-10-741-466-7
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Best Local Similarity 100.
Matches 12; Conservative
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                                                                                     RESULT 12
US-10-741-466-7
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US-10-741-466-8
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                                                                                                                                 Query Match
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 12; Conservative 0; Mismatches 0; Indels
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Sequence 6, Application US/10741466

Publication No. US20040180058A1

GENERAL INFORMATION:
APPLICANT: Sherman, M.
APPLICANT: Sherman, M.
TITLE OF INVENTION: Vaccine Compositions and Methods
FILE REFRENCE: 25855-003
CURRENT FILING DATE: 2003-12-19
PRIOR FILING DATE: 2002-12-20
NUWBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 309
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FUDDICATION NO. US20040180354A1
GENERAL INFORMATION:
APPLICANT: Sinard, John J. L.
APPLICANT: Diamond, David C.
APPLICANT: Liu, Liping
TITLE OF INVENTION: EPITOPE SEQUENCES
FILE REFERENCE: MANK.032A
CURRENT APPLICATION UNMBER: US/10/657,022
CURRENT FILING DATE: 2003-09-04
PRIOR FILING DATE: 2003-09-06
NUMBER OF SEQ ID NOS: 610
SOFTWARE: FABELSEQ for Windows Version 4.0
SEQ ID NO 71
LENGTH: 309
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; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-71
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US-10-657-022-71
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Best Local Similarity
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US-10-657-022-71
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100.0%; Score 57; DB 12; Length 3541;
Best Local Similarity 100.0%; Pred. No. 0.095;
Matches 12; Conservative 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Melanoma cancer specific savine
US-10-296-734-1454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 129, Application US/10117937
FUBLICATION NO. US2003022023911
GENERAL INFORMATION:
APPLICANT: CTL IMMUNO THERAPIES CORP.
APPLICANT: SIMARD, John, J.L.
APPLICANT: DIAMOND, David, C.
APPLICANT: LIU, Liping
APPLICANT: LIU, Liping
APPLICANT: LIU, Liping
APPLICANT: ALA CALLON OF SEQUENCES
FILE OF INVENTION: EPTTOPE SEQUENCES
FILE REFERENCE: CTLIMM.027A
CURRENT APPLICATION NUMBER: US 60/282,211
PRIOR APPLICATION NUMBER: US 60/282,211
PRIOR APPLICATION NUMBER: US 60/337,017
PRIOR APPLICATION NUMBER: US 60/337,017
PRIOR APPLICATION NUMBER: US 60/337,017
PRIOR APPLICATION NUMBER: US 60/337,017
PRIOR APPLICATION NUMBER: US 60/337,017
PRIOR APPLICATION NUMBER: US 60/337,017
PRIOR PLING DATE: 2001-10-07
PRIOR APPLICATION NUMBER: US 60/363,210
PRIOR APPLICATION NUMBER: US 60/363,210
PRIOR APPLICATION NUMBER: US 60/363,210
PRIOR APPLICATION NUMBER: US 60/363,210
PRIOR APPLICATION NUMBER: US 60/363,210
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PRIOR APPLICATION NUMBER: US 60/363,210
PRIOR APPLICATION NUMBER: US 60/363,210
PRIOR APPLICATION NUMBER: US 60/363,210
PRIOR APPLICATION NUMBER: US 60/363,210
CURRENT FILING DATE: 2003-08-04
PRIOR PAPLICATION NUMBER: AU PQ7761/00
PRIOR FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 1507
SEQ ID NO 1454
LENGTH: 3541
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Best Local Similarity 100.
Matches 10; Conservative
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; ORGANISM: Homo sapiens
US-10-117-937-129
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Search completed: October 7, 2004, 15:33:47 Job time : 44.7273 secs

1 YVIKVSARVR 10

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GenCore version 5.1.6.
(c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein

October 7, 2004, 15:17:11; Search time 13.9091 Seconds (without alignments) 82.989 Million cell updates/sec Run on:

US-09-336-091-7 57 Title: Perfect score:

1 EYVIKVSARVRF 12 Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283366 Total number of hits satisfying chosen parameters:

283366 segs, 96191526 residues

Searched:

seq length: 0 seq length: 200000000 Minimum DB e Maximum DB e

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:\*

Database

1: pirl:\* 2: pir2:\* 3: pir3:\* 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	melanoma antigen M	hypothetical prote	fatty-acid synthas	hypothetical prote	conserved hypothet	aspartyl-tRNA synt	aspartate-tRNA lig	1-phosphatidylinos	aspartyl-tRNA synt	hypothetical prote	conserved hypothet	hypothetical prote	leucine aminopepti	hypothetical prote	probable preprotei	titin, cardiac mus	probable iron-sulf	protein T4012.19 [	probable membrane	hypothetical prote		conserved hypothet	aspartate-tRNA lig	large T antigen -	hypothetical prote		ppsl protein - Myc	hypothetical prote	DNA-directed RNA p
SUMMARIES	ID	138661	H71122	S61703 ·	S72753	F72265	G81195	F81831	A54600	E83524	D83036	AE2832	A97610	H70479	S57974	H84721	I38344	S19343	D96788	S56777	T24822	C75316	G69317	AE2110	TVVPMK	H70871	A86983	S72760	T01460	B95229
	DB	5	~	~	~	~	N	~	Н	~	~	~	N	~	~	~	-4	~	~	~	~	~	7	7	-	~	~	7	~	N
	Query Match Length	317	357	1887	392	594	602	602	1070	591	255	288	317	493	534	556	26926	497	118	323	355	450	538	595	649	846	869	869	946	1225
d¥	Query Match	68.4	64.9	64.9	63.2	63.2	63.2	63.2	63.2	61.4	59.6	59.6	59.6	59.6	59.6	59.6	59.6	58.8	57.9	57.9	57.9	57.9	57.9	57.9	57.9	57.9	57.9	57.9	57.9	57.9
	Score	39	37	37	36		36			35	34	34	34	34	34	34	34	33.5	33	33	33	33	33	33	33	33	33	33	33	33
	Result No.	7	8	Э	4	S	9	7	89	σ	10	11	12	13	14	15	16	17	18.	19	50	21	22	23	24	25	56	27	28	29

C;Superfamily: tumor associated protein MAGE F;169-177/Region: HLA-A1 binding #status predicted

A; Introns: #status absent

DNA-directed RNA p	hypothetical prote	hypothetical prote	fatty-acid synthas	collagen alpha 1(V	titin - rabbit (fr	hypothetical prote	transcription regu	rho protein GDP-di	rho protein GDP-di	histone H1.3 - Cae	hypothetical 24.5K	hypothetical prote	methyltransferase	probable dipeptide	succinate dehydrog
F98093	F86436	T16860	JC4086	A54849	S20901	E72309	F82611	S12121	138156	T16138	JN0060	T01614	E69303	F71036	E84360
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1225	1253	1357	1885	2944	6805	33	126	204	204	208	230	263	270	278	318
57.9	57.9	57.9	57.9	57.9	57.9	56.1	56.1	56.1	56.1	56.1	56.1	56.1	56.1	56.1	56.1
33	33	33	33	33	33	32	32	32	32	32	32	32	32	32	32
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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Immunogenetics 40, 360-369, 1994
A;Title: Structure, chromosomal localization, and expression of 12 genes of the MAGE far
A;Reference number: I38659; MUID:95012457; PMID:7927540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: 138662
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: 138662
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-172, TT, 174-317 <DEP2>
A;Cross-references: EMBL:U10688; NID:g533516; PIDN:AAA68872.1; PID:g533517
A;Cross-references: EMBL:U10688; NID:g533516; PIDN:AAA68872.1; PID:g533517
A;Cross-references: EMBL:U10688; NID:g533516; PIDN:AAA68872.1; PID:g533517
A;Exp. Med. 176, 1453-1457, 1992
A;Exp. Med. 176, 1453-1457, 1992
A;Exp. Med. 176, 1453-1457, 1992
A;Exp. Med. 176, 1453-1457, 1992
A;Exp. Mulp:g3018875; PMID:1402688
A;Accession: PH1297
                                                                                 C;Species: Homo sapiens (man)
C;Date: 07-Jun-1996 Hagquence revision 07-Jun-1996 #text_change 18-Feb-2000
C;Accession: 138661; H3862; FH1297; PH1298; JC2359; G01446
R;De Plaen, E.; Arden, K.; Traversari, C.; Gaforio, J.J.; Szikora, J.P.; De Smet, C.;
                                                                                                                                                                                                                                                                                                                                                                                                                          A;Accession: I38661
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Nolcoule type: DNA
A;Residues: 1-317 <DEP1-
A;Residues: 1-317 <DEP1-
A;Cross-references: EMBL:U10687; NID:g533514; PIDN:AAA68871.1; PID:g533515
A;Experimental source: antigen MAGE-4a
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A;Residues: 1.172, TT',174-306,'Q',308-317 <DIN>
A;Cresidues: EMBL:U10340; NID:9499123; PIDN:AAA19007.1; PID:9499124
A;Experimental source: melanoma cell line DM150
                                        41 protein; melanoma antigen MAGE-X2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 169-172, 'T', 174-177 < TRA2>
A; Experimental Source: antigen MAGE-41
R; Ding, M; Beck, R.J.; Keller, C.J.; Fenton, R.G.
Biochem. Biophys. Res. Commun. 202, 549-555, 1994
A; Title: Cloning and analysis of MAGE-1-related genes.
A; Reference number: JC2358; MUID:94311935; PMID:8037761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Residues: 169-177 <TRA1>
A,Experimental source: antigen MAGE-4
- human
melanoma antigen MAGE-4
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Fri Oct

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A; Gene: SGD: FAS2
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                                                                                                                                                                                                                                                                                                                                                                                                       C)Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 02-Feb-2001
C;Accession: H71122
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekir R;Kawarabayasi, Y.; Sawada, M.; Horikawa, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Reference number: A71000; MUID:98344137; PMID:979942.1; PID:97957159
A;Reference number: GB:AP000003; MID:97336130; PIDN:BAA29842.1; PID:97357159
A;Reference this accession replaces an interim accession for a sequence replaced by GenBank C;Genetics:
A;Genet: this accession replaces an interim accession for a sequence replaced by GenBank C;Genetics:
A;Gene: PH0751
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RiUrrestarau, L.A.; Vissers, S.
submitted to the Protein Sequence Database, May 1996

A;Reference number: S6251

A;Accession: S65256

A;Molecule type: DNA

A;References: EMBL:Z3587; NID:g1370477; PIDN:CAA97948.1; PID:g1370478; MIPS:YPL23

A;Experimental acurce: strain S288C (ABP22)

R;Rieger, M.; Mueller-Auer, S.; Schaefer, M.

submitted to the Protein Sequence Database, May 1996
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N;Alternate names: protein P1409; protein YPL231w
C;Species Saccharomyces cerevisiae
C;Date: 09-Mar-1996 #sequence revision 12-Apr-1996 #text_change 20-Jun-2000
C;Accession: S61703; S65256; S65250; A31107
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A;Reference number: S61699
A;Rocession: S61703
A;Molecule type: DnA
A;Rocesside: 1-1887 <URR>
A;Rocesside: 1-1887 <URR>
A;Cross-references: EMBL:X94561; NID:g1181252; PIDN:CAA64256.1; PID:g1181257
                                                                                                         Gaps
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A.Experimental source: strain S288C (AB972)
R.Mohamed, A.H.; Chirala, S.S.; Mody, N.H.; Huang, W.Y.; Wakil, S.J.
J. Biol. Chem. 263, 12315-12325, 1988
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                                    Length 317;
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                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein PH0751 - Pyrococcus horikoshii
                                       DB 2;
                                    Score 39; DB 2
Pred. No. 3.3;
4; Mismatches
                                    68.4%;
63.6%;
Query Match
Best Local Similarity 63.07
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                                                                                                                                                                 1 EYVIKVSARVR 11
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A;Accession: 865250
A;Molecule type: DNA
A;Residues: 1567-1887 <RIE>
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Best Local Similarity
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R; Urrestarazu, L.A.
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A;Molecule type: DNA
A;Rebidues: 1-310, 'TTGTGG',311-593,'I',595-940,'CLNCVKSWLKLLKKLERQFPSKLLW','SIRLSWAIALMLi
A;Cross-references: EMBL:J03936; NID:g171501; PIDN:AAA34601.1; PID:g171502
C;Genetics:
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C;Ganetics:
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C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: F72265
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sec A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sec A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: F72265
A;Status: preliminary
A;Residues: preliminary
A;Residues: 1-594 cARN>
A;Residues: 1-594 cARN>
A;Cross-references: GB:AE001788; GB:AE000512; NID:g4981893; PIDN:AAD36406.1; PID:g498189
A;Title: Primary structure of the multifunctional alpha subunit protein of yeast fatty A;Reference number: A31107; MUID:88315020; PMID:2900835 A;Accession: A31107
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C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 23-Mar-2001
C;Accession: S72753; T11012
R;Smith, Dr.R; Roblison, K.
Bubmitted to the EMBL Data Library, November 1993
A;Description: Mycobacterium leprae cosmid B1496.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-392 <SMI>
A; Residues: 1-392 <SMI>
A; Cross-references: EMBL: U00013; NID:9466868; PIDN:AAA17119.1; PID:9466874
R; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
R; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
A; Reference number: 216918
A; Reference number: 216918
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from A; Residues: 1-392 <PAR>
A; Residues: 1-392 <PAR>
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Pred. No. 18;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
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                                                                                                                                                                                                                                                                      A, Cross-references: SGD:S0006152; MIPS:YPL231w
A, Map position: 16L
S. Superfamily: yeast fatty-acid synthase
C, Keywords: acyltransferass; coenzyme A
                                                                                                                                                                                                                                                                                                                                                                                                                                     64.9%; Score 37;
88.9%; Pred. No.
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70.0%;
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Best Local Similarity 70.0
Matches 7; Conservative
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Best Local Similarity
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1-phosphatidylinositol 3-kinase (EC 2.7.1.137) 110K chain beta isoform - human C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C.Accession: A54600
R.Hu, P.; Mondino, A.; Skolnik, B.Y.; Schlessinger, J.
A.H. Ell Biol. 13, 777-7688, 1993
A.Title: Cloning of a novel, ubiquitously expressed human phosphatidylinositol 3-kinase A; Reference number: A54600; MUID:94067128; PMID:8246984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: E83524
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; B
Adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim
indury, S.; Olson, M.V.
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A;Accession: E83524
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A;Molecule type: DNA
A;Residues: 1-591 <STO>
A;Cross-references: GB:AE004530; GB:AE004091; NID:g9946865; PIDN:AAG04352.1; GSPDB:GN00
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C.Jate: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C.Accession: D83036
R.Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   - Pseudomonas aeruginosa (strain PAO1)
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                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-1070 cHUI>
A;Cross-references: GB:S67334; NID:g455759; PIDN:AAB29081.1; PID:g455760
A;Note: sequence extracted from NCBI backbone (NCBIN:140879, NCBIP:140880)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Pred. No. 49;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 591;
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5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Cross-references: GDB:136233
C,Superfamily: phosphatidylinositol 3-kinase
C,Keywords: phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61.4%; Score 35; 45.5%; Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aspartyl-tRNA synthetase PA0963 [imported]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63.2%;
50.0%;
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C;Superfamily: lysine-tRNA ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :||::|| || :
245 DYVLQVSGRVEY 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 50.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EYVIKVSARVRF 12
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EFVVKITGKVR 77
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                             66 EYVLSITGRVR 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Genetics:
A;Gene: GDB:PIK3CB; PIK3C1
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D83036
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                                                                                                                                                                                                                                                                                                                                                                                                                                          asparryl-tRNA synthetase NMB0466 [imported] - Neisseria meningitidis (strain MC58 serogr C; Species: Neisseria meningitidis C; Species: Natseria meningitidis C; Species: Natseria meningitidis C; Date: 31-Mar-2000 #text_change 19-Jan-2001 C; Accession: G81195  
R; Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; Mite, O.; Fleischmann, R.D.; Dougherty, B.A.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. A; Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, B.R.; Rappuoli, R.; Ve A; Reference number: A81000; MUD:2017575; PMID:10710307  
A; Reference number: A81000; MUD:2017575; PMID:10710307  
A; Residues: preliminary A; Molecule type: DNA A; Residues: 1-602 < TET.> A; Cross-references: GB:AE002403; GB:AE002098; NID:g7225688; PIDN:AAF40903.1; PID:g722569 A; Experimental source: serogroup B, strain MC58 A; Experimental source: serogroup B, strain MC58 A; Experimental source: serogroup B, strain MC58
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R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel Holtoy, S.J.; Churcher, C.; Klee, S.R.; Morel Holtoy, S.J.; Agels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491.
A;Reference number: A81775; MUD:2022556; PMID:10761919
A;Status: preliminary
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*Residues: 1-602 cPAR-
A;Cross-references: GB:AL162757; GB:AL157959; NID:g7380371; PIDN:CAB85238.1; PID:g738064
A;Experimental source: serogroup A, strain 22491
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                                                                                                                                            Length 594;
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                                                                                                                                      Score 36; DB 2;
Pred. No. 27;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.2%; Score 36; DB 2; llarity 54.5%; Pred. No. 27; Conservative 3; Mismatches
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A;Experimental source: strain MSB8
C;Genetice:
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C,Superfamily: lysine-tRNA ligase
C,Keywords: ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Superfamily: lysine-tRNA ligase
                                                                                                                                      63.2%;
63.6%;
                                                                                                                                Query Match
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                    289 EYIIKKGGRVR 299
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66 EYVLSITGRVR 76
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Best Local Similarity
Matches 6; Conserv
                                                    C;Genetics:
A;Gene: TM1334
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Gaps

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4; Indels

Length 317;

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A,Residues: 1-493 <AQF>
A,Cross-references: GB:AE000772; NID:g2984299; PIDN:AAC07829.1; PID:g2984306; GB:AE00065
A,Experimental source: strain VF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                        R; Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-534 «MUR>
A;Cross-references: EMBL:Z50046; NID:g899393; PID:g899397; GSPDB:GN00004; MIPS:YDR147w
A;Experimental source: strain AB972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 392, 353-358, 1998
AyItile: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: H70479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
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NyAlternate names: hypothetical protein YD8358.04
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 13.-Jan.1996 #sequence_revision 01-Mar-1996 #text_change 19-Apr-2002
C;Accession: S77974
R;Wurphy, L.; Rtchards, C.; Harris, D.
A;Reference number: S57971
                                                                                                                                                                                                                                                                                                                                                          Species: Aquifex aeolicus
| Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 03-Mar-2003
| Accession: H70479
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Pred. No. 63;
2; Mismatches
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Pred. No. 58;
                                                 Score 34; DB 2;
Pred. No. 37;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                  leucine aminopeptidase - Aquifex aeolicus
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C,Superfamily: Cytosol aminopeptidase
  A, Map position: circular chromosome
                                                       59.6%;
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ilarity 58.3%;
Conservative
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A;Cross-references: SGD:S0002554
A;Map position: 4R
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                                                                                                           6; Conservative
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EYIMKVSSNV 493
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                                                    Query Match
Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 7; Conserv
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A; Molecule type: DNA
                                                                                                                                                                                                                    195
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S57974
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                                                                                                A; Accession: D83036
A; Status: preliminary
A; Status: preliminary
A; Medicule type: DNA
A; Residues: 1-255 <STO>
A; Cross-references: GB: AE004901; GB: AE004091; NID: g9951147; PIDN: AAG08267.1; GSPDB: GN001
C; Genetics:
A; Gene: P84882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein AGR_C_3779 [imported] - Agrobacterium tumefaciens (strain C58, Cere C;Species: Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002 C;Accession: A97610 R;Godner, B.; Hinkle, G.: Gattung S · Millar N · Dianaters C.
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Science 294, 2323-2328, 2001
A; Fittle: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A; Reference number: A97359; MUID:21608551; PMID:11743194
..; Lory, S.; Olson, M.V.
Mature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
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A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-288 «KURA
A; Cross-references: GB: AE008688; PIDN: AAL43075.1; PID: g17740544; GSPDB: GN00186
A; Experimental source: strain C58 (Dupont)
C; Genetics:
A; Genetics: A; A; App. ABA
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C;Date: 11-Jan_2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Datce: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: H4721
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
W.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nisterman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Rocession: H84721
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-556 <STO>
A;Cross-references: GB:AE002093; NID:g4582448; PIDN:AAD24832.1; GSPDB:GN00139
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A;Map position: 2
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Search completed: October 7, 2004, 15:18:18 Job time : 14.9091 secs

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                     Schultz-Thater E., Juretic A., Dellabona P., Luscher U., Siegrist W., Harder F., Heberer M., Zuber M., Spagnoli G.C.; "MAGE-1 gene product is a cytoplasmic protein."; Int. J. Cancer 59:435-439(1994).
                                                                            development and tumor transformation or aspects of tumor progression. Antigen recognized on a melanoma by autologous cytolytic T lymphocytes subscribing. Subscribing LOCATION: Cytoplasmic. TISSUE SPECIFFCITY: Expressed in many tumors of several types, such as melanoma, head and neck squamous cell carcinoma, lung carcinoma and breast carcinoma, but not in normal tissues except
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10-OCT-2003 (Rel. 42, Last annotation update)
Melanoma-associated antigen 4 (MAGE-4 antigen) (MAGE-X2) (MAGE-41)
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                                                                                                                                                         for testes. Never expressed in kidney tumors, leukemias and
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                                                       Int. J. Cancer 59:435-439(1994).
-!- FUNCTION: Not known, though may play a role in embryonal
                                                                                                                                                                                                                                                                                                                                                                                                                               T -> A (probable polymorphism).
/FTId=VAR 004283.
R -> Q (in dbSNP:2008144).
/FTId=VAR 011737.
D->A: ABOLISHES HLA-A1 BINDING.
Y->A: ABOLISHES HLA-A1 BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50838; MAGE; 1.
Antigen; Multigene family; Polymorphism; Tumor antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  544EEB1F9F4E9D33 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 57; DB 1; L
100.0%; Pred. No. 0.00038;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 317 AA.
                                                                                                                                                                                                                                                                                          SIMILARITY: Contains 1 MAGE domain.
                                                                                                                                                                                                                                                                                                                                                                                                                      POLY-SER.
          MEDLINE=95012905; PubMed=7927954;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ·
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1995 (Rel. 32, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34342 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       281 EYVIKVSARVRF 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EYVIKVSARVRF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                       36
                                                                                                                                                                                                                                                                                                                                                                                                                                                       72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163 1
169 1
309 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAGEA4 OR MAGE4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAG4 HUMAN
                                                                                                                                                                                                                                                                                                                                                                                               Antigen; 1
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P43358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAG4_HUMAN
                                                                                                               <del>+</del> +
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ò
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Tissuescent R., Chomez P., de Backer D., Cavenee W., Boon T.;

Resistent R., Chomez P., de Backer D., Cavenee W., Boon T.;

E. TOWNER E. Milhomosomal localization, and expression of 12 genes of the The Thomas F. (2019).

Resistent R. Milhoms P., de Backer D., Cavenee W., Boon T.;

R. MISTURES-SAINSTS, PubMed-801761;

R. MISTURES-SAINSTS, PubMed-101761;

R. MISTURES-SAINSTS, PubMed-101761;

R. MISTURES-SAINSTS, PubMed-101761;

R. MISTURES-SAINSTS, PubMed-101761;

R. MISTURES-SAINSTS, PubMed-1017761;

R. MISTURES-SAINSTS, PubMed-1017761;

R. MISTURES-SAINSTS, PubMed-1017732;

R. MISTURES-SAINSTS, PubMed-1017733;

R. MISTURES-SAINSTS, PubMed-10177733;

R. MISTURES-SAINSTS, PubMed-1017733;

R. MISTURES-SAINSTS,
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NON TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                 SYD_PSESM
                                                                                                                                                                                  ò
                                                                                                                                                                                                                            음
                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SECRAINS—NCD 1674;
MEDLINE=97016803; PubMed=8863429;
MEDLINE=97016803; PubMed=8863429;
MOTER R., Collins M.D., O'Hanlon K., Wallbanks S., Richardson P.T.;
Morse R., Collins M.D., O'Hanlon K., Wallbanks S., Richardson P.T.;
"Analysis of the beta' subunit of DNA-dependent RNA polymerase does
not support the hypothesis inferred from 165 rRNA analysis that
Oenococcus oeni (formerly Leuconostoc oenos) is a tachytelic
(fast-evolving) bacterium.";
Int. J. Syst. Bacteriol. 46:1004-1009(1996).

-IFUNCTION: DNA-dependent RNA polymerase catalyzes the transcription
of DNA into RNA using the four ribonucleoside triphosphates as
                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
DNA-directed RNA polymerase beta' chain (EC 2.7.7.6) (Transcriptase beta' chain) (RNA polymerase beta' subunit) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - {NNA}(N).
-1- SUBUNIT: The enzyme consists of the sigma chain and the core enzyme which is composed of 2 alpha chains, 1 beta chain, beta' chain.
-1- SIMILARITY: Belongs to the RNA polymerase beta' chain family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                               ;
0
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InterPro; IPR007080; RNA pol Rpbl 1.
InterPro; IPR007080; RNA pol Rpbl 1.
InterPro; IPR007083; RNA pol Rpbl 3.
InterPro; IPR007083; RNA pol Rpbl 4.
InterPro; IPR007083; RNA pol Rpbl 4.
InterPro; IPR006592; RNA pol Rpbl 1.
InterPro; IPR006592; RNA pol Rpbl 1.
InterPro; IPR006593; RNA pol Rpbl 1.
InterPro; IPR006593; RNA pol Rpbl 1.
InterPro; IPR006693; RP0LA N; I.
InterPro; IPR007698; RNA pol Rpbl 1.
InterPro; IPR007698; RNA pol RNA pol Merase; Transcription.
                                                                                                                                                                        Score 39; DB 1; Length 317;
Pred. No. 2;
1; Mismatches 0; Indels
                                                 T -> A.
/FTId=VAR_004284.
E -> Q (IN REF. 2).
3CFAC0E2B696257C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oenococcus oeni (Leuconostoc oenos).
Bacteria, Firmicutes; Lactobacillales; Oenococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1004 AA
  MAGE.
POLY-SER.
                                                                                                                            317 AA; 34929 MW;
                                                                                                                                                                           68.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X96384; CAA65248.1; -. HSSP; Q9KWU6; 1HQM.
                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                       |:|::|:|||
289 EHVVRVNARVR 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                             EYVIKVSARVR 11
                                                                                                                                                                                                  Local Similarity
les 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=1247;
  110
41
173
                                                                                                       307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      RPOC OENOE
                                                                                                  CONFLICT
DOMAIN
DOMAIN
VARIANT
                                                                                                                                                                           Query Match
                                                                                                                                                                                                       Best Loca
Matches
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InterPro; IPR004115; GAD dom.
InterPro; IPR004136; ENNA-synt_2.
InterPro; IPR004365; ENNA-synt_asp.
InterPro; IPR004365; LRNA_anti_
Ffam; PF02393; GAD; 1.
Ffam; PF01336; LRNA_anti; 1.
Ffam; PF01336; LRNA_anti; 1.
Pfam; PF01336; LRNA_anti; 1.
Pfam; PF01336; LRNA_anti; 1.
Pfam; PF01316; PS0862; AAA_TRNA_IIGASE II; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                               15-WAR-2004 (Rel. 43, Created)
15-WAR-2004 (Rel. 43, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Aspartyl-tRNA synthetase (EC 6.1.1.12) (Aspartate--tRNA ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas syringae (pv. tomato).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                  ö
                                                                  DB 1; Length 1004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64.9%; Score 37; DB 1; Length 591;
                                                                                                               1; Indels
                       73750DF47F3A2C36 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66351 MW; 4A841555305FBF36 CRC64;
                                                                                          6.5;
                                                                                                                                                                                                                                                                                                                            591 AA.
                                                                                       Pred. No. 6.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diphosphate + L-aspartyl-tRNA(Åsp).
-!- SUBUNIT: Homodimer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
                                                                    Score 39;
                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22834015; PubMed=12928499;
1004 1004
1004 AA; 111965 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE016870; AAO57440.1; -.
                                                                                          63.6%;
                                             Query Match
Best Local Similarity 63.0
Servative 7; Conservative
                                                                                                                                                                                                     942 EYVLPISARLR 952
                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                          1 EYVIKVSARVR 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PSPT03981; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              591 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Asprs).
Asps or pspto3981.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=323;
                                                                                                                                                                                                                                                                                                                       SYD PSESM
Q87<u>Y</u>31;
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Contract to

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g
      STRAIN=5288C / AB972;

MEDLINE=97313271; PubMed=9169875;

MEDLINE=97313271; PubMed=9169875;

MEDLINE=97313271; PubMed=9169875;

A araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V.,

A araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V.,

Chung B., Churcher C.M., Coster F., Davis R.W.,

Dietrich F.S., Delius H., DiPaolo T., Dubois B., Duesterhoeft A.,

Duncan M., Floeth M., Fortin N., Friesen J.D., Fritz C., Goffeau A.,

Hall J., Hebling U., Heumann K., Hilbert H., Hillier L.W.,

Hall J., Hebling U., Heumann K., Hilbert H., Hillier L.W.,

Komp C., Kurdi O., Lashkari D., Lew H., Lin A., Lin D., Louis B.J.,

Marathe R., Messenguy F., Mewes H.-W., Mirtipati S., Moestl D.,

Muller-Auer S., Namath A., Nentwich U., Oeffer P., Pearson D.,

Noetel F.X., Pohl T.W., Purnelle D., Schafer M., Schafer M.,

Scherens B., Schramm S., Schroeder M., Sdicu A.M., Tettelin H.,

Urrestearazu L.A., Ushinsky S., Vierendeels F., Vissers S., Voss H.,

Walsh S.V., Wambutt R., Wandy Y., Wedler E., Wedler H., Winnett E.,

Zhong W.W., Zollner A., Vo D.H., Hani J.;

"The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI.";
                  ö
                                                                                                                                                          P19097; 01253; 01-NOV-1990 (Rel. 16, Created) 28-FBB-2003 (Rel. 41, Last sequence update) 10-OCT-2003 (Rel. 42, Last annocation update) Fatty acid synthase subunit alpha (EC 2.3.1.86) [Includes: Acyl carrier; 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) (Beta-ketoacyl reductase); 3-oxoacyl-[acyl-carrier protein] synthase (EC 2.3.1.41) (Beta-ketoacyl synthase);
                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Cerulenin-resistant mutants of Saccharomyces cerevisiae with an altered fatty acid synthase gene.";
Mol. Gen. Genet. 244:90-96(1994).

-!- FUNCTION: Fatty acid synthetase catalyzes the formation of long-chain fatty acids from acetyl-CoA, malonyl-CoA and NADPH.

The alpha subunit contains domains for: acyl carrier protein, loxoacyl-[acyl-carrier protein] synthase. This subunit coordinates the binding of the six beta subunits to the enzyme complex.
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=88315020; PubMed=2900835;
Mohamed A.H., Chirala S.S., Mody N.H., Huang W.Y., Wakil S.J.;
Primary structure of the multifunctional alpha subunit protein of yeast fatty acid synthase derived from FAS2 gene sequence.";
J. Biol. Chem. 263:12315-12325(1988).
                                                                                                                                                                                                                                                                                  FAS2 OR YPL231W OR P1409.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetels;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inokoshi J., Tomoda H., Hashimoto H., Watanabe A., Takeshima H.,
                  ô
                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                  PRT; 1887 AA.
                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=5288c;
MEDLINE=94316198; PubMed=8041367;
                  2;
63.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 387:103-105(1997).
                Conservative
                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MUTAGENESIS OF GLY-1250.
                                              1 EYVIKVSARVR 11
                                                               |||:|| :||
67 EYVVKVVGKVR 77
 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=X2180-1A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schueller H.J.
                                                                                                                                                  YEAST
               Matches
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                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BETA-KETOACYL SYNTHASE (BY SIMILARITY).
G-S: CERULENIN-RESISTANCE.
G -> GTGTGG (IN REF. 1).
T -> I (IN REF. 1).
AKLRKELVETSEVRKAVSIETALEHKVVNGNSADAAYAQVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IQPRANIQLDFPELKPYKQVKQIAPAELEGLLDLERVI -> CLNCVKSWLKLLKLERQFPSKLLWSIRLSMAIALMLHMLKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R GETINIALIUS: TITLES:

R GETINIALIUS: TITLES:

R INTERPRO! IPR0008278; 4-PPT_transf.

R INTERPRO: IPR0008278; 4-PPT_transf.

R INTERPRO: IPR000184; Ketcacyl synth.

R INTERPRO: IPR000162; Pantethn_trn.

R FEAM: PF01648; ACPS: 1.

R FOSSITE: PS000012; PH0SPHOPANTETHEIRS: 1.

R PROSITE: PS000012; PHOSPHOPANTETHEIRS: 1.

R PROSITE: PS00006; B KETCACYL SYNTHASE; 1.

R PROSITE: PS00006; B MILITURCTIONAL CARRIER (ACP).

KW Transferase; NADP; Phosphopantetheine.

FT DOWAIN 675 874 BETA-KETCACYL RYNTHASE.

FT DOWAIN 675 874 BETA-KETCACYL RYNTHASE.

FT BINDING 189 180 PHOSPHOPANTETHEIR (RY SYNTHASE).

FT BINDING 180 180 PHOSPHOPANTETHEIR (RY SYNTHASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KFNQELTFNWTSQNRNHTNRLNKLLPLSLRVCWIWKELF
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CATALYTIC ACTIVITY: Acetyl-CoA + N malonyl-CoA + 2N NADPH = a long-chain acyl-CoA + N CoA + N CO(2) + 2N NADP(+).

CATALYTIC ACTIVITY: Acyl-[acyl-carrier protein] + malonyl-[acyl-
                                                                                                          [acyl-carrier protein].
-!- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein]
NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
-!- SUBUNIT: [Alpha(6)beta(6)] hexamers of two multifunctional subunits (alpha and beta).
-!- SIMILARITY: TO THE FATTY ACID SYNTHETASE, SUBUNIT ALPHA FROM
                                                                                  carrier protein] = 3-oxoacyl-[acyl-carrier protein] + CO(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RWEMEA -> KMGNGS (IN REF. 1).
A -> S (IN REF. 1).
N -> T (IN REF. 1).
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(Rel. 36, Last sequence update)
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EMBL, X76890; CAA54258.1; --
EMBL, X34561; CAA64256.1; --
EMBL, Z73586; CAA97947.1; --
EMBL, Z73586; CAA97947.1; --
PIR, S61703; S61703.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64.98;
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Best Local Similarity 86.>
8. Conservative
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1671
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YE62 MYCLE
ID YE62 MYCLE
AC Q49682;
DT 15-UUL-1998 (
DT 15-UUL-1998 (
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MUTAGEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AL162757; CAB85238.1; -.

R HSRSP; P21889; LECN
R HSRSP; P21889; LECN
R HAMAP; MF 00044; -: 1.

InterPro; IPR0041524; AspS bact.
R InterPro; IPR004364; LRNA-synt_2.
R InterPro; IPR004364; LRNA-synt_2.
R InterPro; IPR004365; LRNA-synt_asp.
R InterPro; IPR004365; LRNA-synt_2.
R InterPro; IPR004365; LRNA-ligase_II.
R Pfam; PF00152; LRNA-synt_2.
R Pfam; PF00152; LRNA-synt_2; 2.
R Pfam; PF01365; LRNA-synt_2; 2.
R Pfam; PF01365; LRNA-synt_2; 2.
R R Pfam; PF01365; LRNA-synt_2; 2.
R R Pfam; PF01425; LRNA-synt_2; 2.
R R Pfam; PF01645; LRNA-synt_1; 1.
R RINTS; PR01045; ANA-LIGASE_II; 1.
R ROSITE; PS50862; AA FRNA_LIGASE_II; 1.
A Minoacyl-tRNA synthetase; ProteIn biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nelson K.E.,
                                                                                                                                                                                                                                                                                                                        diphosphate + L-aspartyl-tRNA(Asp).
-!- SUBUNIT: Homodimer (By similarity).
-!- SUBCELLUTAR LOCATION: Cytcoplasmic.
-!- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
                    Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd (aggels K.M., Leather S., Monle S., Mungall K., Quail M.A.,
Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
Whitehead S., Spratt B.G., Barrell B.G.,
"Complete DNA sequence of a serogroup A strain of Neisseria
meningitidis Z2491.";
Nature 404:502-506(2000).
-!- CATALYTIC ACTIVITY: ATP + L-aspartate + LRNA(Asp) = AMP +
James K.D., Bentley S.D., Churcher C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Aspartyl-tRNA synthetase (EC 6.1.1.12) (Aspartate--tRNA ligase)
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STRAIN=MCS8 / Serogroup B;
MEDLINE=20175755; PubMed=10710307;
Tettelin +, Saunders N.J., Heidelberg J., Jeffries A.C., Nels
Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neisseria meningitidis (serogroup B).
Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63.2%; Score 36; DB 1; Length 602; 54.5%; Pred. No. 16; 2; Indels 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             602 AA; 67976 MW; EF41A56255A79491 CRC64;
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NCBI TaxID=491,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
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EYVLSITGRVR 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Ruther S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R., Barrell B.G.;
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09JT23;
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
ABPATLY1-LRNA synthetase (EC 6.1.1.12) (Aspartate--tRNA ligase)
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                                                                                                      Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1769;
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ASPS OR NWA2019.
Asps on meningitidis (serogroup A).
Bacteria; Protobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 392;
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                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Smith D.R., Robison K.;
Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interpro; IPR000825; UPF0051.
Pfam; PF01458; UPF0051; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 392 AA; 42202 MW; 891162F7CA494C6A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
-!- SIMILARITY: Belongs to the UPF0051 (ycf24) family.
                              Hypothetical protein ML0594.
ML0594 OR MLCL536.27C OR U1496A OR B1496_C1_154.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 36; DB 1;
Pred. No. 10;
2; Mismatches
28-FEB-2003 (Rel. 41, Last annotation update)
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MEDLINE=20222556; PubMed=10761919;
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EMBL; AL583919; CAC30102.1; -.
PIR; S72753; S72753.
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                                                                                                   Mycobacterium leprae.
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Best Local Similarity
Matches 7; Conserv
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SEQUENCE

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SMART;
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Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Gill J., Sarlato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
115-MAR-2004 (Rel. 43, Last annotation update)
Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit, beta isoform (EC 2.7.1.153) (Pl3-kinase pl10 subunit beta) (Ptdins-3-kinase pl10) (Pl3K) (Pl3Kbeta).
                                                                                                           -i - CATALYTIC ACTIVITY: ATP + L-aspartate + tRNA(Asp) = AMP + diphosphate + L-aspartyl-tRNA(Asp).
-i - SUBUNIT: Homodimer (By similarity).
-i - SUBCELLULAR LOCATION: Cytoplasmic.
-i - SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGRFAMS; TIGRO0459; aspS bact; 1.
PROSITE; PS50862; AA_TRNA_LIGASE II; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.2%; Score 36; DB 1; Length 602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    602 AA; 68124 MW; 5DC8A016B0C13E3C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-94067128; PubMed-8246984;
Hu P., Mondino A., Skolnik E.Y., Schlessinger J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1070 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 16;
3; Mismatches
                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                               HAMAP, MF 00044; -; 1.
InterPro; IPR004524; AspS bact.
InterPro; IPR004115; GAD dom.
InterPro; IPR004934; NucTeic acid OB.
InterPro; IPR004364; tRNA-synt_2.
InterPro; IPR004365; tRNA-synt_asp.
InterPro; IPR004365; tRNA-anti.
InterPro; IPR004365; tRNA-anti.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF02938; GAD; 1.
Pfam; PF01352; tRNA-synt_2; 2.
Pfam; PF01336; tRNA_anti; 1.
PRINTS; PR01042; TRNASYNTHASP.
                                                                                                                                                                                                                                                                                     EMBL; AE002403; AAF40903.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ilarity 54.5%;
Conservative
                                                                                                 Science 287:1809-1815(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EYVIKVSARVR 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EYVLSITGRVR 76
                                                                                                                                                                                                                                                                                              PIR; G81195; G81195.
HSSP; P21889; 1EQR.
TIGR; NMB0466; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome
SEQUENCE 602 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIK3CB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P11B_HUMAN
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Matches
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M. GO. (1901) 19. Propaphatidylinositol 3-kinase activity; TAS.

GO. (20.000187; P. Pactivation of MAPK; TAS.

GO. (20.0000187; P. Pactivation of MAPK; TAS.

R. (20.0000187; P. Pactivation of MAPK; TAS.

GO. (20.000074; P. Pactivation of Cell cycle; TAS.

R. (20.000074; P. Pacqulation of Cell cycle; TAS.

R. (2
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                                                                                                                                                                                                                                                                             Kossila M., Sinkovic M., Karkkainen P., Laukkanen M.O., Miettinen R., Kossila M., Sinkovic M., Karkkainen P., Laukkanen M.O., Miettinen R., Rissanen J., Kekalainen P., Kuusisto J., Yla-Hertutala S., Laakso M.; "Gene encoding the catalytic subunit pilobeta of human phosphatidylinositol 3-kinase: cloning, genomic structure and screening for variants in patients with type 2 diabetes."; submitted (AUG-2000) to the EMBL/GenBank/DDBA databases.
-!- FUNCTION: PHOSPHORYLATES PTDINS, PTDINS4P AND PTDINS (4,5) P2 WITH PREFERENCE FOR PTDINS (4,5) P2.
-!- CATALYTIC ACTIVITY: ATP + 1-phosphatidyl-1D-myo-inositol 4,5-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- PATHWAY: Signaling pathways regulating cell growth.
-!- SUBUNIT: HETERODIMER OF A P110 (CATALYTIC) AND A P85 (REGULATORY)
"Cloning of a novel, ubiquitously expressed human phosphatidylinositol 3-kinase and identification of its binding site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bisphosphate = ADP + 1-phosphatidyl-1D-myo-inositol 3,4,5-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- TISSUE SPECIFICITY: Expressed ubiquitously.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00915; PI3.4_KINASE_1; 1. PROSITE; PS00916; PI3.4_KINASE_2; 1. PROSITE; PS50290; PI3.4_KINASE_3; 1. Transferase; Kinase; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMEL, AJ297549, CAC21449.1, EMEL, AJ297550, CAC21449.1, JOINED. EMEL, AJ297551, CAC21449.1, JOINED. EMEL, AJ297551, CAC21449.1, JOINED. EMEL, AJ297553, CAC21449.1, JOINED. EMEL, AJ297555, CAC21449.1, JOINED. EMEL, AJ297556, CAC21449.1, JOINED. EMEL, AJ297559, CAC21449.1, JOINED.
                                                                                                                                                                         Cell. Biol. 13:7677-7688(1993).
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SWART; SM00143; PI3K P85B; 1.
SWART; SM00144; PI3K rbd; 1.
SWART; SM00145; PI3Ka; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; S67334; AAB29081.1; -.
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MIM; 602925; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A54600; A54600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           trisphosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT.
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Transferase, Kinase, Multigene family
DOMAIN 800 1050 P13K/P141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR004364; tRNA-synt 2
                                                                                                                                                                                                                                                                                                       SYD_PSEAE
Q51422;
                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                 (AspRS)
                                                                                                                          Matches
                                                                                                                                                                                                                                                                                    SYD_PSEAE
                                                                                                                                                                  ò
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                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit, beta
isoform (EC 2.7.1.153) (PI3-kinase pll0 subunit beta) (Ptdins-3-kinase
pll0) (PI3K) (PI3Kbeta).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ⋖
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- PATHWAY: Signaling pathways regulating cell growth.
--- SUBUNIT: HFTERODIMER OF A P110 (CATALYTIC) AND A P85 (REGULATORY)
SUBUNIT (BY SIMILARITY: Belongs to the P13/P14-kinase family.
                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Mětazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                     ;
                                                        Score 36; DB 1; Length 1070;
Pred. No. 29;
4; Mismatches 2; Indels
                  1070 AA; 122762 MW; 81135FE93452C00E CRC64;
                                                                                                                                                                                                                                                                                  PRT; 1070 AA.
  PI3K/PI4K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam, PF00613; P13Kā; 1.

SWART; SW00142; P13K C2; 1.

SWART; SW00144; P13K C2; 1.

SWART; SW00144; P13K rbd; 1.

SWART; SW00145; P13Ka; 1.

PROSITE; PS00915; P13 4 KINASE 1; 1.

PROSITE; PS50290; P13 4 KINASE 2; 1.

PROSITE; PS50290; P13 4 KINASE 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR008973; C2 Calb.
InterPro; IPR00403; P13 P14 kinase.
InterPro; IPR002403; P13K C2.
InterPro; IPR003113; P13K_D85B.
InterPro; IPR003113; P13K_ras_bind.
InterPro; IPR001263; P13Kas_bind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00454; PT3 PT4 kinase; 1. Pfam; PF00792; PT3K C2; 1. Pfam; PF00192; PT3K P65B; 1. Pfam; PF00794; PT3K Pbd; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AJ012482; CAA10046.1; -.
                                                                                                                                                                                                                                                                                                                          (Rel. 40, Created)
                                                      63.2%;
50.0%;
                                                                                                                                                                :||::|| ||:
245 DYVLQVSGRVEY 256
                                                                                                   6; Conservative
                                                                                                                                         1 EYVIKVSARVRF 12
                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR008938; ARM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
  1050
                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               trisphosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                        16-OCT-2001
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                P11B RAT
Q9Z1LO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                PIK3CB.
                                                                                                   Jatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-ATCC 15692 / PAO1;
MEDLINE-20437337; Pubmed-10984043;
STRAIN-ATCC 15692 / PAO1,
SCOVER C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
Garber R.L., Goltry L., Tolentino B., Westbrock-Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ruvA, ruvB
                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Aspartyl-tRNA synthetase (EC 6.1.1.12) (Aspartate--tRNA ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97136691; PubMed=8982068; Hishida T., Iwasaki H., Ishioka K., Shinagawa H.; Molecular analysis of the Pseudomonas aeruginosa genes, ruvA and ruvC, involved in processing of homologous recombination intermediates.";
                                                                                Score 36; DB 1; Length 1070;
Pred. No. 29;
4; Mismatches 2; Indels
                    1070 AA; 122607 MW; 4E8EB2333E96E4D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                        591 AA
PI3K/PI4K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acid OB.
                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAMAP, MF_00044; -; 1.
InterPro; IRR004524; AspS bact.
InterPro; IPR004115; GAD Gom.
InterPro; IPR008994; Nucleic_ac:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE004530; AAG04352.1; -. EMBL; D83138; BAA11815.1; -. EPIR; B83524; E83524. PIR; PC4295; PC4295. HSSP; P21889; 1EQR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 231-591 FROM N.A. STRAIN-ATCC 15692 / PAO1;
                                                                                   63.2%;
                                                                                                              50.08;
                                                                                                                                                                                                                                   :||::|| || :
245 DYVLQVSGRVEY 256
                                                                                                                                         6; Conservative
                                                                                                                                                                                                  1 EYVIKVSARVRF 12
                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        opportunistic pathogen."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 406:959-964(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas aeruginosa.
                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=287;
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CAEEL
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                                                                                                                                                                                                                                                                                                                                                               ö
                  InterPro; IRR064365; FRNA_ingase_II.
InterPro; IRR064365; FRNA_ligase_II.
Ffam; PF02338; GAD; 1...
Pfam; PF021316; FRNA_anti; 1.
Pfam; PF011316; FRNA_anti; 1.
PRINTS; PR01042; FRNA_SYNTHASP.
FIGRRAMs; TGR00459; aspS_bact; 1.
PROSITE; PS50862; AA_TRNA_LIGASE_II; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

MEDLINE=22423060; PubMed=12534463;
Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
Nation Gos Santos V.A.P., Fours D.E., Gill S.R., Pop M., Holmes M.,
Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,
Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,
Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzez A.,
Utterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H.,
Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
                                                                                                                                                                                                                                                                                                                                                               .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-WAR-2004 (Rel. 43, Created)
15-WAR-2004 (Rel. 43, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Aspartyl-tRNA synthetase (EC 6.1.1.12) (Aspartate--tRNA ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                            61.4%; Score 35; DB 1; Length 591; 45.5%; Pred. No. 25; ive 5; Mismatches 1; Indels
                                                                                                                                                                                                                                              P -> A (IN REF. 2).
; 62B278CA0EDE70A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              591 AA
InterPro; IPR002312; tRNA-synt_asp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HAMAP; MF_00044; -; 1.
InterPro; IPR004115; GAD_dom.
InterPro; IPR0043164; tRNA-synt_2.
InterPro; IPR004365; tRNA-synt_asp.
InterPro; IPR004365; tRNA-anti.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudomonas putida (strain KT2440)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=160488;
                                                                                                                                                                                                                                                                   66207 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE016778; AAN66837.1; -.
                                                                                                                                                                                                                                                                                                                                                             5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                             |:|:|:|
EFVVKITGKVR 77
                                                                                                                                                                                                                                                                                                                                                                                                      1 EYVIKVSARVR 11
                                                                                                                                                                                                                                                                     591 AA;
                                                                                                                                                                                                                            Complete proteome.
                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYD_PSEPK
ID SYD_PSEPK
AC Q88NJ4;
                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                      ö
Pfam; PF02938; GAD; 1.
Pfam; PF00152; tRNA-synt_2; 1.
Pfam; PF00152; tRNA-synt_2; 1.
PRINTS; PR01042; TRNASYNTHASP.
PROSTTS; PS50862; AA TRNA LIGASE II; 1.
Aminoacyl-tRNA synthetase; Proteïn biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISOId=09U332-2; Sequence=VSP 007365;
Note=No experimental confirmation available;
-!- SIMILARITY: Belongs to the L31E family of ribosomal proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RMEL; Z82077; CAB63351...
REMEL; Z82077; CAB63351...
ROTHERPO; W09CS.6b; CE20168.
DR NormPep; W09CS.6b; CE20169.
DR ProDom; PRO0198; Ribosomal L316., 1.
DR PROSITE; PS01144; RIBOSOMAL L316; 1.
DR Ribosomal protein; Alternative splicing.
Ribosomal protein; Alternative splicing.
Missing (in isoform b).
"TRAPELIC 1 52 /FITG=VSP 007365.
"TATG=VSP 007365.
"TATG=VSP 007365.
"TATG=VSP 007365.
"TATG=VSP 007365."
                                                                                                                                                                                                                                                                 61.4%; Score 35; DB 1; Length 591;
45.5%; Pred. No. 25;
iive 5; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lennard N.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                            591 AA; 66568 MW; B823515D39E52E0F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name-a;
IsoId=Q9U332-1; Sequence=Displayed;
Note=No experimental confirmation available;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RL31_CAEEL STANDARD; PRT; 122 AA. 09U332; 09U331; 110-0CT-2003 (Rel. 42, Created) 10-0CT-2003 (Rel. 42, Last sequence update) 10-0CT-2003 (Rel. 42, Last annotation update) 60S ribosomal protein L31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 34; DB
Pred. No. 7.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REVISIONS, AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59.6%;
                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                           1 EYVIKVSARVR 11
                                                                                                                                                                                                                                                                                                                                                                                                                                    67 EYVVQITGKVR 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
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                                                                                                                                                                                   Complete proteome
SEQUENCE 591 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RPL-31 OR W09C5.6
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                                                                                                                                                                                                                                                                          Query Match
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Probable cytosol aminopeptidase (EC 3.4.11.1) (Leucine aminopeptidase) (Leucyl aminopeptidase).
                        PEPA OR AQ 2099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACT_SITE
ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 100:9388-9393 (2003).

-!- FUNCTION: Associates with the EF-Tu.GDP complex and induces the exchange of GDP to GTP. It remains bound to the aminoacyl-tRNA.EF-Tu.GTP complex up to the GTP hydrolysis stage on the ribosome.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to the EF-Ts family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FROM EF-
 Gaps
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINE=22784745; PubMed=12886019;

Gil R., Silva F.J., Zientz B., Delmotte F., Gonzalez-Candelas F.,
Latorre A., Rausell C., Kamerbeek J., Gadau J., Hoelldobler B.,
Latorre A., Aross R., Moya A.;

"The genome sequence of Blochmannia floridanus: comparative analysis of reduced genomes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; ant endosymbionts; Candidatus Blochmannia.
NCBI_TaxID=203907;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; Processive British Pfam; Processive British Profesors Fig. 1.
PROSITE; PS01126; EF TS 1; 1.
PROSITE; PS01127; EF TS 2; 1.
PROSITE; PS01127; EF TS 2; 1.
Elongation factor; Protein biosynthesis; Complete proteome.

Blongation factor; Protein biosynthesis; Complete proteome.

TU (BY SIMILARITY).

TO (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 34; DB 1; Length 269;
Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
 3.
                                                                                                              15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
17-17-18-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                           PRT;
                                                                                                                                                                                                 Candidatus Blochmannia floridanus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAMAP; MF 00050; -; 1.
InterPro; IPR001816; EF TS.
InterPro; IPR000449; UBA_domain.
Pfam; PF00889; EF TS; 1.
Pfam; PF00627; UBA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     252 EYCIKINNFVRF 263
Conservative
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les 7; Conservative
                                                                                                             STANDARD;
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                      1 EYVIKVSARVR 11
                                     || | : [|:|
EYTIHIHARIR 30
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16-OCT-2001
28-FEB-2003
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                                                                                                           EFTS CANBE
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067868;
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                                                                                                 CANBF
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Matches
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similarity).
CATALYTIC ACTIVITY: Release of an N-terminal amino acid, Xaa-|-Xbb-, in which Xaa is preferably Leu, but may be other amino acids including Pro although not Arg or Lys, and Xbb may be Pro.
COFACTOR: Binds 2 manganese ions per subunit (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: Belongs to peptidase family M17.

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                                                                                                                                                                                                                                                                                                                                                                                     Nature 392:353-358(1998).
-1- FUNCTION: Presumably involved in the processing and regular turnover of intracellular proteins. Catalyzes the removal of unsubstituted N-terminal amino acids from various peptides (By
                                                                                                                                                                                                                       Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Garbham D.E., Overbeek R., Shead M.A., Keller M., Aujay M., Huber Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Manganese; Complete proteome.
MANGANESE 2 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 (BY SIMILARITY).
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                       Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex
NCBI_TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A32B499C7A52065B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MERCES; M17.UPW; -...
HAWAP; MF 00181; -; 1.
HAMAP; MF 00181; -; 1.
InterPro: IPR000813; Peptidase M17_C.
InterPro: IPR000813; Peptidase M17_N.
Pfam; PF00883; Peptidase M17; I.
PRINTS; PR00481; LAWNOPPIDASE.
PROSITE; PS00631; CYTOSOL AP; 1.
Hydrolase; Aminopeptidase; Manganese; Cc.
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                                                                                                                                                                                        MEDLINE=98196666; PubMed=9537320;
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484 EYIMKVSSNV 493
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HSSP; P00727; 1LAP.
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341
341
269
343
493 AA;
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Aquifex aeolicus.
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Opzrn4 chimpanzee
Opngp3 homo sapien
O98my2 rhizobium 1
O9c114 pasteurella
O9c124 pasteurella
O9c124 fusobacterides
O8r624 fusobacteri
O8r624 fusobacteri
O8r624 fusobacteri
O8r639 synechococo
C88839 encephalito
O8J89 tropheryma
O90yv3 ictalurus p
O8z201 pyrobaculum
O9dby1 ictalurus p
O8z201 pyrobaculum
O9dby1 vibrio vuln
O9dby1 vibrio vuln
O9dby1 vibrio vuln
O9dby1 sapeudomonas
O8f9y1 septospira
O7vre5 candidatus
O8ee18 shewanella
O9G809 myxoma viru
O9G901 shope fibro
O91k3 bacillus ce
                                                                                                                                                                                                                                                                    Q81is3 bacillus ce
Q9siq4 arabidopsis
Q8ryg5 oryza sativ
Q875e4 podospora a
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUENCE FROM N.A.
TISSUE-Hepatoma;
Sui Y., Ye J., Wu W.;
"Cloning of a new gene of MAGE family in human hepatocellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 57; DB 4; Length 316; 100.0%; Pred. No. 0.0018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    carcinoma."; Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases. Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF441295; AAL37897.1; InterPro; IPR002190; MAGE. InterPro; PR01454; MAGE; 1. PR051TE; PS50038; MAGE; 1. SEQUENCE 316 AA; 35409 MW; A463A9A740A089DF CRC64;
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Last annotation update)
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Q88NJ4
Q8DJS8
Q83KS9
Q83HS9
Q90YV3
Q80ZBV3
Q8DBV3
Q8DBV3
                                       Q9CL14
Q8A569
Q9DWE8
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Q8F9W3
Q7VRE5
Q8UDN7
Q8EEL8
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Best Local Similarity 100.0%;
Matches 12; Conservative 0
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QBKEIS;
01-OCT-2002 (TrEMBLrel. 22,
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 NCBI_TaxID=9606;
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Q14798 homo sapien
Q9bun9 homo sapien
Q93n48 coxiella bu
Q9igu9 tanapox vir
Q9dhn9 yaba-like d
Q9dhn9 yaba-like d
Q87y31 pseudomonas
Q87y31 pseudomonas
Q87y31 pseudomonas
Q87y31 streptomona
Q9vch1 drosophila
Q9vch1 drosophila
Q9xch1 drosophila
Q9xch1 drosophila
Q8xmb7 streptomeu
Q8xmb7 christoneu
Q8xmb7 coxiella bu
Q9x156 thermotoga
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                                                                    October 7, 2004, 15:14:05 ; Search time 43.3636 Seconds (without alignments) 87.313 Million cell updates/sec
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          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                  protein search, using sw model
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QRESTS
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sp_human: *
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sp_mammal: *
sp_mhc: *
sp_page: *
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sp_plant: *
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Match Length DB
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57
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Perfect score:
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Maximum DB
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Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S., Kounddinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y., Phelan M., Farmer A.; "Cloning of human full-length CDSs in BD Creator (TM) System Donor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
HOOVET T.A., Vodkin M.H., Williams J.C., Culp D.W., Thompson H.A.;
Achromosomal DNA deletion explains the phenotype of the Coxiella
burnetii phase II variant.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE=22608657; PubMed=12704232;
SeshadriR., Paulsen I.T., Eisen J.A., Read T.D., Nelson K.E.,
Nelson W.C., Ward N.L., Tettelin H., Davidsen T.M., Beanan M.J.,
DeBoy R.T., Daugherty S.C., Brinkac L.M., Madupu R., Dodson R.J.
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Coxiellaceae; Coxiella.
NCBI_TaxID=777;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68.4%; Score 39; DB 4; Length 318; 63.6%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Skin antigen, family A, 8 (Melanoma antigen, family A, 8)
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vector.";
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC002455; AAH02455.1; -.
EMBL; BC012744; AAH12744.1; -.
InterProf. IPR002190; MAGE.
Pfam; PF01454; MAGE.
PROSITE; PS50838; MAGE; 1.
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Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                      PRELIMINARY;
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                                                               289 EHVVRVNARVR 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       291 EHVVRVNÁRVR 301
      1 EYVIKVSARVR 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. TISSUE=Skin;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                  STRAIN=TLS / ATCC 49652 / DSM 12025;

MEDLINE=22103665; PubMed=12093901;

A Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,

A Bodson R.J., Deboy K. G'Hum M.L., Nelson W.C., Haft D.H.,

Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F.,

Holt I., Umayam L.A., Mason T., Brenner M., Shea T.P., Parksey D.,

A Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune D.,

Vamathevan J., Khouri H., White O., Gruber T.M., Ketchum K.A.,

Venter J.C., Tettelin H., Bryant D.A., Fraser C.M.;

The complete genome sequence of Chlorobium tepidum TLS, a

photosynthetic, anaerobic, green-sulfur bacterium.";

Proc. Natl. Acad. Scl. U.S.A. 99:9509-9514(2002).
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2003 (TrEMBLrel. 23, Last annotation update)
MAGE-4 protein.
MELANOMA ANTIGEN-4.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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EMBL; D32075; BAA06841.1; -...
Interpro. IPRO0190; MAGE.
PROSITE; PS50838; MAGE; 1.
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                                                                                                                                                       Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68.4%; Score 39; DB 4; Length 317; 63.6%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IndelB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28214 MW; 45382717E1A8A9F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          317 AA; 35044 MW; 9B9477253FE307C4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO, GO:0008237; F:metallopeptidase activity; IEA.
GO; GO:0008270; F:zinc ion binding; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR002725; DUF45.
InterPro; IPR006625; Pept_M_Zn_BS.
Pfam; PF01863; DUF45; 1.
01-OCT-2002 (TrEMBLrel. 22, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3,
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2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   317 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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SEQUENCE 248 AA; 28214 M
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Best Local Similarity 58.3
Matches 7; Conservative
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Best Local Similarity 63.6
Matches 7; Conservative
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14 EYTVKVSQRARY 25
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                                                                  Zinc protease, putative.
                                                                                                                           Chlorobium tepidum.
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                                                                                                                                                                                       Chlorobium.
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Kawarabayasi Y., Kawada M., Horikawa H., Haikawa Y., Hino Y.,
Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
Funañashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
"Complete sequence and gene organization of the genome of a hyper-
thermophilic archaebacterium, Pyrococcus horikoshii OT3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
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                                                                                                                                                                                                                                                                       Gaps
                SEQUENCE FROM N.A.
MEDLINE=21176566; PubMed=11277691;
MEDLINE=21176566; Routh G.L.;
"The genome sequence of Yaba-like disease virus, a yatapoxvirus.";
Virology 281:170-192(2001).
                                                                                                                                      of.
                                                                                                                                  Thesis (2000), Sir William Dunn School of Pathology, University EMBL; AJ293568; CAC21312.1; -. GO; GO: 0019031; C:viral envelope; IEA. InterPro; IPR004900; Pox. P35. Ffam; PF03213; Pox P35; I. SEQUENCE 323 AA; 37354 MW; 9D1111ABC5E19B27 CRC64;
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                                                                                                                                                                                                                                          Length 323;
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                                                                                                                                                                                                                                                                     2; Indels
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EMBL, AP000003; BAA29842.1; -
PIR, H71122; H71122.
InterPro, IRR002831; DUF118.

Prodom, P0006327; DUF118; 1.

Hypothetical protein; Complete proteome.

SEQUENCE 357 AA; 40905 MW; 24BE20213B3C402C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                      64.9%; Score 37; DB 12;
ilarity 54.5%; Pred. No. 29;
Conservative 3; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                       357
                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=013;
MEDLINE=98344137; PubMed=9679194;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein PH0751.
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187 YIIRVSTAIRF 197
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nes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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297 EYPIEVSGRVR 307
                                                                                                                                                                                                                                                                                                  2 YVIKVSARVRF 12
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                                                                                                                                                                                                                          Query Match
Best Local Similarity 5
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                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                        Lee H.J.;
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AC Q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tanapox virus.
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
Yatapoxvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yaba-like disease virus (YLDV).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
Yatapoxvirus.
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Khouri H.M., Lee K.H., Carty H.A., Scanlan D., Heinzen R.A., Thompson H.A., Samuel J.E., Fraser C.M., Heidelberg J.F., "Complete genome sequence of the Q-fever pathogen, Coxiella burnetii.";
                                                                                                                                                                                                                                   68.4%; Score 39; DB 16; Length 458; 54.5%; Pred. No. 16; Ative 5; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 37; DB 12; Length 323;
Pred. No. 29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Essani K., Paulose-Murphy M.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AR74513774.1; -
GO; GO:0019031; C:viral envelope; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lee H.J.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                          ll protein; Complete proteome.
458 AA; 53179 MW; A42FF4615563D648 CRC64;
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Pfam; PF03213; Pox P35; I.
SEQUENCE 323 AA; 37342 MW; A964C9EIDD5880AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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O-MAR-2001 (TrEMBLrel 16, Created)

01-MAR-2001 (TrEMBLrel 16, Last sequence update)

01-JUN-2003 (TrEMBLrel 24, Last annotation update)
                                                           U.S.A. 100:5455-5460(2003)
                                                                                                TIGN; CBU0695; -.
GO; GO: 001649; -.
GO; GO: 001649; F: oxidoreductase activity; IEA.
GO; GO: 0016418; F: electron transport; IEA.
InterPro; IPR065797; Cytb b6_N.
PROSITE; P800192; CYTCORROME B. HBME; 1.
PROTHECT I Drotein; Complete Protecome
SEQUENCE 458 AA; 53179 MW; A42FP4615563D648
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                                                       Proc. Natl. Acad. Sci. U.S.A. 1
EMBL, AF387640, AAK71274.1; -.
EMBL, AE016962; AAO90239.1; -.
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54.5%;
                                                                                                                                                                                                                                                                6; Conservative
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187 YIIRVSTAIRF 197
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7 KYLIKIAARIR 17
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                    Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=99000;
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CG10192 protein.
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Q9VCH1
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                                                                                                                                                                                                                                     Berry K., Joardar V., Khouri H., Fedorova N., Tran B., Russell D., Berry K., Utterback T., Van Aken S., Feldblyum T., Gwinn M., Dodson R., Deboy R., Durkin A., Kolonay J., Madupu R., Daugherty S., Bannan M., Haft D., Selengut J., Nelson W., Davidsen T., White O., Fraser C., Collmer A.; "Complete sequence of Pseudomonas syringae."; Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases. EMBL; AE016870; AAOS7440.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                                                                                    Pseudomonas syringae (pv. tomato).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
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Pfam; PF0135; tRNA-synt_2; 1.
Pfam; PF01345; tRNA-snti; 1.
PRINTS; PR01042; TRNASYNTHASP.
PROSITE; PS0862; AA TRNA_LIGASE II; 1.
Aminoacyl-tRNA synthetase; Complete proteome.
SEQUENCE 591 AA; 66351 MW; 4A841555305FBF36 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                   TIGR; PSPT03981; -...
GO; GO:0005737; C:cycoplasm; IEA.
GO; GO:0004815; F:aspartate-trNA ligase activity; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0003676; P:nucleic acid binding; IEA.
GO; GO:0006422; P:asparty]-tRNA aminoacylation; IEA.
                      Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation updat. Aspartyl-tRNA synthetase. ASPS OR PSPT03981.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64.9%; Score 37; DB 63.6%; Pred. No. 53; ive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro, IPR004115, GAD_dom.
InterPro, IPR008994; Nucleic_acid_OB.
InterPro, IPR004364; tRNA-synt_2.
InterPro, IPR002312; tRNA-synt_asp.
InterPro, IPR004365; tRNA_anti.
InterPro, IPR006195; tRNA_anti.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        llarity 63.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
tes 7; Conserv
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                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                         NCBI_TaxID=323;
                                                                                                                                                                                                                       STRAIN=DC3000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loc
Matches
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DDT BERNAM OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOC
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RC STRAIN-BECKELEY;

RX MEDLINE-20196006; Dubbed=10731132;

RA Adams N.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D. Celniker S.E., Holt G. Malson C.R., Miklos G.D.,

RA Adams M.D. Lewis S.E., Richards S., Abburner M., Henderson S.N.,

RA Gorger R.A., Lewis S.E., Richards S., Abburner M., Henderson S.N.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeliffer B.D.,

RA Abril J.F. Agbayan A., An H.-J., Andrews-Pfannkoch C.R., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beaaley E.M.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beaaley E.M.,

RA Borkova D., Borcham R.R., Bouck J., Brokstein P., Brottier P.,

RA Borkova D., Borcham R.P., Bouck J., Brokstein P., Brottier P.,

RA Ghofon R., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Gloden R., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Gloden R., Doup L.E., Downes M., Dugan-Rocha S., Durkov B.C., Dunn P.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

Harris N.L., Harvey D., Hahman T.J., Herrandez J.R., Houck J.,

RA Harris N.L., Haveton R.K., Howland T.J., Wei M.-H., Ibegwam C.,

Alalli M., Kalush F., Karpten G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Alalli M., Kalush F., Karpten G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Ra Mount S.M., Moy M., Murphy E., Murphy L., Muzny D.M., Nelson D.L.,

Reinert K., Remington K.A., Howland T.S., Walpski M.P., Shuh H.,

Raben D.R., Nelson K.A., Howland T.S., Walpski M.P., Shuh T.,

Spier E., Spradling A.C., Stapheron M., Strong R., Sun E.,

Syradling R., Sender-Kiamos I., Simpson M., Strong R., Walsenbach J.,

RA Shiers R., Tectro C., Turner R., Venter E., Wang K., Walsenbach J.,

Walls A. R., Wooley E., Romington K.A., Walsenbach J.,

RA Williams S.M., Woodage T., Worley C., Wang G., Zhan R.,

RA Shen S., Tectro C., Turner R., Venter E., Wang G., Zhan R.,

Ra Anner K., Shen R.-P., Zaveri J.S., Zhan M., Shup S., Zhu X., Zhu S., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         64.9%; Score 37; DB 5; Length 933; 77.8%; Pred. No. 83; 0; Indels Live 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha
Ephydroidea, Drosophilidae, Drosophila
                                                                     INTERPRO; IPRO08938; ARM.
INTERPRO; IPRO08938; ARM.
INTERPRO; IPRO03890; IF e1F4G.
INTERPRO; IPRO03891; IF-E1F4G_MA3.
Pfam; PF02854; MA3; 1.
Pfam; PF02854; MA5; 1.
SWART; SM00544; MA5; 1.
SWART; SM00543; MIF4G; 1.
SEQUENCE 933 AA; 106862 MW; GADFDBF51C566543 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
GO; GO:0003723; F:RNA binding; IEA.
GO; GO:0006412; P:protein biosynthesis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 77.0.
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Barrett J.W., Krell P.J., Arif B.M.,
                             SEQUENCE FROM N.A.
     NCBI_TaxID=33903;
                                                                                                                                    metabolites.";
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                                               Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,

Barane C.A., Gocayne J.D., Amanatides P.G., Racandon R.C., Rogers Y.,

Barane C.A., Gocayne J.D., Amanatides P.G., Racandon R.C., Rogers Y.,

Banzon J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,

Rerriera S., Frise E., Galle R.F., Garg N.S., George R.A.,

Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

McIntosh T.C., Moy M., Murphy B.A., Nelson C., Nelson K.A., Nunco J.,

Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,

Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,

Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;

"Sequencing of Drosophila melanogaster genome.",

Submitted (WAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                          Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
Tupy J.L., Bergman B., Carlson J.W., Celniker S.E.,
Tupy J.L., Bergman B., Carlson J.W., Celniker S.E.,
Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
Searle S.M.J., Smith B., Shu S., Smutniak F., Whitfield E.,
Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 37; DB 5; Length 2072;
Pred. No. 1.8e+02;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SMO0544; MA3; 1.
SMART; SMO0543; MIF4G; 1.
SEQUENCE 2072 AA; 226597 MW; A&DEF55D5B3F25D8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
Gibbs R.A., Myers B.W., Rubin G.M., Venter J.C., "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE003745; ARF56194.2; -...
FlyBase; FBGN0039122; CG10192.
GO; GO:0003723; F:RNA binding; IEA.
GO; GO:0006412; P:protein biosynthesis; IEA.
InterPro; IPR008938; ARM.
InterPro; IPR003890; IF eIF4G.
InterPro; IPR003891; IF_eIF4G_MA3.
Pfam; PF02847; MA3, 1.
Pfam; PF02847; MRF4G; 1.
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Best Local Similarity 77.0
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MEDLINE-95297142; PubMed-7778276; Xie W.D. D., Arif B., Dobos P., Krell P.J.; "Identification and analysis of a putative origin of DNA replication in the Choristoneura fumiferana multinucleocapsid nuclear polyhedrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Liu J.J., Carstens B.B.; "Identification, localization, transcription, and sequence analysis of the Choristoneura fumiferana nuclear polyhedrosis virus DNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                   Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T., Sakaki Y., Hattori M., Omura S., "Complete genome sequence and comparative analysis of the industrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                 Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C., Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T., Kikuchi H., Shiba T., Sakaki Y., Hattori M.; "Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lee H.Y., Arif B., Dobos P., Krell P., Identification of bent DNA and ARS fragments in the genome of Choristoneura fumiferana nuclear polyhedrosis virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Choristoneura fumiferana nuclear polyhedrosis virus (CfMNPV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63.2%; Score 36; DB 16; Length 176; 70.0%; Pred. No. 26; ive 2; Mismatches 1; Indels
STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165; MEDLINE=21477403; PubMed=11572948;
                                                                                                                                                                                                                                                                                                                                                        STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=22608306; PubMed=12692562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6AA9343933A30366 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viruses; dsDNA viruses, no RNA stage; Baculoviridae, Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              microorganism Streptomyces avermitilis.";
Nat. Biotechnol. 21:526-531(2003).
EMBL; AP005028; BAC69454.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein, Complete proteome.
SEQUENCE 176 AA; 19152 MW; 6AA934393
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MEDLINE=95297155; PubMed=7778286;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               our-2003 (TERMELE1. 25, 01-0CT-2003 (TERMELE1. 25, Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Virus Res. 24:249-264(1992).
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les 7; Conservative
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115 VLKVAARTRF 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 VIKVSARVRF 12
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409 4
409 AA;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                       Qiu W., Liu J.J., Carstens E.B.; "Studies of Choristoneura fumiferana nuclear polyhedrosis virus gene
                                                                                                                                                                                                                                                                                                                                                                                                                                      SECUENCE FROM N.A. MEDIMEd=10814576; MEDLINE=20276145; PubMed=10814576; Lapointe R., Back D.W., Ding Q., Carstens E.B.; Indentification and molecular characterization of the Choristoneura funiferana multicapsid nucleopolyhedrovirus genomic region encoding the regulatory genes pkip, p47, lef-12, and gta."; virology 271:109-121(2000).
"Characterization, sequencing and phylogeny of the ecdysteroid UDP-glucosyltransferase gene from two distinct nuclear polyhedrosis viruses isolated from Choristoneura fumiferana.";
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MEDLINE=2185455; PubMed=11864738;
Caratena B.B., Liu J.J., Dominy C.;
Cardentification and molecular characterization of the baculovirus
CfMNPV early genes: ie-1, ie-2 and pe38.";
Virus Res. 83:13-30(2002).
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to phosphatidylinositol 3-kinase, catalytic subunit, beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63.2%; Score 36; DB 12; Length 259; 63.6%; Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R., Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases. EMBL, BC039650; AAH39650.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleopolyhedrovirus.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF512031; AAP29898.1; -.
Hypothetical protein.
SEQUENCE 259 AA; 31288 MW; 1508ED2257534DIE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
                                                                                                          SEQUENCE FROM N.A.
MEDLINE=96183379; PubMed=8610448;
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                                                                                                                                                                                                  insect cells.";
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Best Local Similarity
7; Conserva
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria, Proteobacteria, Gammaproteobacteria, Legionellales,
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Pred. No. 60;
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Last annotation update)
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                                                                                                                                                                                                                                                                         63.2%;
50.0%;
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239 DYVLQVSGRVEY 250
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SQ SEQUENCE 590 AA; 66754 MW; 33E3AD62742969C8 CRC64;
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0; Gaps Query Match 63.2%; Score 36; DB 16; Length 590; Best Local Similarity 70.0%; Pred. No. 86; Matches 7; Conservative 2; Mismatches 1; Indels

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